

DO NOT REMOVE
Send to Applicant

QY 1320 TTTAAAAAAAAAAAAAAAAAAAA 1346
 DB 1383 TCAATTGTGAAAAAAAAAAAAAAAA 1409
 RESULT 210
 ID AAZ65261 standard; DNA, 1447 BP.
 AC AAZ65261;
 DT 23-MAR-2000 (first entry)
 DE Human secreted protein gene 12.
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; ds.
 OS Homo sapiens.
 PN W09958660-A1.
 PD 18-NOV-1999.
 PF 06-MAY-1999; 99WO-US009847.
 PR 12-MAY-1998; 98US-0085093P.
 PR 12-MAY-1998; 98US-0085094P.
 PR 12-MAY-1998; 98US-0085105P.
 PR 12-MAY-1998; 98US-0085180P.
 PR 18-MAY-1998; 98US-0085906P.
 PR 18-MAY-1998; 98US-0085920P.
 PR 18-MAY-1998; 98US-0085921P.
 PR 18-MAY-1998; 98US-0085922P.
 PR 18-MAY-1998; 98US-0085923P.
 PR 18-MAY-1998; 98US-0085924P.
 PR 18-MAY-1998; 98US-0085925P.
 PR 18-MAY-1998; 98US-0085927P.
 PR 18-MAY-1998; 98US-0085928P.
 PA (HMO-) HUMAN GENOME SCI INC.
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW;
 PI Endress GA, Ebner R;
 DR WPI, 2000-062296/05.
 DR P-PSDB; AAY76135.
 XX New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX Claim 1; Page 303; 475bp; English.
 CC AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
 CC AAY76124 to AAY76233 represent the secreted proteins encoded by the 97
 CC human genes. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.
 CC by protein or gene therapy. Also pathological conditions can be diagnosed
 CC by determining the amount of the new polypeptides in a sample or by
 CC determining the presence of mutations in the new genes. Specific uses are
 CC described for each of the 97 genes, based on which tissues they are most
 CC highly expressed in, and include developing products for the diagnosis or
 CC treatment of cancer, tumours, developmental abnormalities and foetal
 CC deficiencies, blood disorders, diseases of the immune system, autoimmune
 CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
 CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,

atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, CC digestive/endocrine disorders, infections and AIDS. The polypeptides are CC also used for identifying their binding partners. The sequences shown CC in AAY6224 to AAY76424 represent fragments of the secreted proteins

XX Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other:

Query Match 98.4%; Score 1324.6; DB 3; Length 1447;
Best Local Similarity 99.3%; Pred. No. 3.5e-258;
Matches 1338; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

```

Oy 1 GAAAGATGTGTGCTGCTCTTTTCTGTGATCTCCATTCATGCTGAATCTGTCAA 60
Db 71 GAAAGATGTGTGCTGCTCTTTTCTGTGATCTCCATTCATGCTGAATCTGTCAA 130
Oy 61 CCAAGTGCAGAAAATGCTTTTAAAGTGAAGCTTATGTCAGAAAGCTCTGGAGATAA 120
Db 131 CCAAGTGCAGAAAATGCTTTTAAAGTGAAGCTTATGTCAGAAAGCTCTGGAGATAA 190
Oy 121 GCATATGCTGGATGCAATGCAAGAAATCTCTTCAAGGATGAGCTTCTCCATG 180
Db 191 GCATATGCTGGATGCAATGCAAGAAATCTCTTCAAGGATGAGCTTCTCCATG 250
Oy 181 AGAAAAGTCCCAAGAGAGCAAGAAATTTCCATGCTCTTCAATGTAAC 240
Db 251 AGAAAAGTCCCAAGAGAGCAAGAAATTTCCATGCTCTTCAATGTAAC 310
Oy 241 CAGAGGTATCATTTGCTTGTGCTTCAAGACCTTCAAAAATACACCTCTCCGT 300
Db 311 CAGAGGTATCATTTGCTTGTGCTTCAAGACCTTCAAAAATACACCTCTCCGT 370
Oy 301 GTTGAAGTGCATACGCTATAGAAATGCAAGAACCGGATCAAAATGCTTCTTA 360
Db 371 GTTGAAGTGCATACGCTATAGAAATGCAAGAACCGGATCAAAATGCTTCTTA 430
Oy 361 AATGACCAAACTGTGAATTTTAAAAATCCCTTCCACTTGCACCAACCCATGACCA 420
Db 431 AATGACCAAACTGTGAATTTTAAAAATCCCTTCCACTTGCACCAACCCATGACCA 490
Oy 421 TCTGTGCAATCTGATTAATTAATTTGTGATTAATTTGATCATCATAGTTCAT 480
Db 491 TCTGTGCAATCTGATTAATTAATTTGTGATTAATTTGATCATCATAGTTCAT 550
Oy 481 GCACTACGATTTTATCAGGATCTGCAAGTGAAGAAAGAAAGAAACCATCTGA 540
Db 551 GCACTACGATTTTATCAGGATCTGCAAGTGAAGAAAGAAAGAAACCATCTGA 610
Oy 541 GTGATGACGCTGAAGATAGTGAAGAAACATGATCACAATTTGAAATGCGCTCT 600
Db 611 GTGATGACGCTGAAGATAGTGAAGAAACATGATCACAATTTGAAATGCGCTCT 670
Oy 601 GATCCCTCGACATGAAGAGG-GGGCATTAATGATGCTTCAATGACAGAGATGAGAG 659
Db 671 GATCCCTCGACATGAAGAGGAGGAGCATTAATGATGCTTCAATGACAGAGATGAGAG 730
Oy 660 CTCACCCCTCTCTGAAGGCTGTGTCTGCTCTCTCAAGAAATTAACATTTGTTCTG 719
Db 731 CTCACCCCTCTCTGAAGGCTGTGTCTGCTCTCTCAAGAAATTAACATTTGTTCTG 790
Oy 720 TGTGATCTGAGATCTGAAATACCAAGAGCAATCAATTTTGTTCACCAATCT 779
Db 791 TGTGATCTGAGATCTGAAATACCAAGAGCAATCAATTTTGTTCACCAATCT 850
Oy 780 TCTTTGTATTAATTTTGAATGCTTGAAGTGAAGAAAGCATCATTAACCAACCA 839
Db 851 TCTTTGTATTAATTTTGAATGCTTGAAGTGAAGAAAGCATCATTAACCAACCA 910
Oy 840 CACCACTGAATCATAGCTATTCAGACTCAAAATATTTCTAATATTTTCTGACGT 899
Db 911 CACCACTGAATCATAGCTATTCAGACTCAAAATATTTCTAATATTTTCTGACGT 970
Oy 900 ATAGTATTAATGCTGATGCTGATTTGATTAATGATTAAGCATTTTGAAT 959

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Db 971 ATAGTATTAATGCTGATGCTGATTTTGAATTAATGATTAAGCATTTTGAAT 1030
Oy 960 AAGATCAGGATATGATTAATTTTCACTTCAAGAAAGCTTGAAGAAATTAATTTCC 1019
Db 1031 AAGATCAGGATATGATTAATTTTCACTTCAAGAAAGCTTGAAGAAATTAATTTCC 1090
Oy 1020 AGTGAAGATTAATTAATGCTGATTAATGCTTGAAGAAATGCTTGTGACATC 1079
Db 1091 AGTGAAGATTAATTAATGCTGATTAATGCTTGAAGAAATGCTTGTGACATC 1150
Oy 1080 ACTATATCATCTGTATATGCTAAGTAAACAAAGTGAAGATTAATTAATG 1139
Db 1151 ACTATATCATCTGTATATGCTAAGTAAACAAAGTGAAGATTAATTAATG 1210
Oy 1140 ATGATTAATTAATGATTAATCAATGATGAGGATTTTATCTGTTATGACAC 1199
Db 1211 ATGATTAATTAATGATTAATCAATGATGAGGATTTTATCTGTTATGACAC 1270
Oy 1200 AGTTGATTAATTTTCTGATTAATCAAGCCCTTAATAGGCAATTCATTTGACAT 1259
Db 1271 AGTTGATTAATTTTCTGATTAATCAAGCCCTTAATAGGCAATTCATTTGACAT 1330
Oy 1260 TTCTCAATTTGTAAGTCCATCTGTGCTAATTAATTAAGTAAATATCATCTCTT 1319
Db 1331 TTCTCAATTTGTAAGTCCATCTGTGCTAATTAATTAAGTAAATATCATCTCTT 1390
Oy 1320 TAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1346
Db 1391 TGAATGCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1417

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RESULT 211
ADE11650
ID ADE11650 standard; cDNA; 1447 BP.
XX
AC ADE11650;
XX
DT 29-JAN-2004 (first entry)
XX
DB Human secreted polypeptide cDNA #12.
XX
KW Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
XX Alzheimer's disease; human; ss; gene.
XX
OS Homo sapiens.
XX
PN US2003100051-A1.
XX
PD 29-MAY-2003.
XX
PF 10-SEP-2001; 2001US-00948783.
XX
PR 12-MAY-1998; 98US-0085093P.
XX 12-MAY-1998; 98US-0085094P.
XX 12-MAY-1998; 98US-0085105P.
XX 12-MAY-1998; 98US-0085180P.
XX 12-MAY-1998; 98US-0085906P.
XX 12-MAY-1998; 98US-0085920P.
XX 12-MAY-1998; 98US-0085922P.
XX 12-MAY-1998; 98US-0085923P.
XX 12-MAY-1998; 98US-0085924P.
XX 12-MAY-1998; 98US-0085925P.
XX 12-MAY-1998; 98US-0085927P.
XX 12-MAY-1998; 98US-0085928P.
XX 06-MAY-1999; 99WO-US009847.
XX 10-NOV-1999; 99US-00437658.
XX 11-SEP-2000; 2000US-0231846P.
XX 28-JUN-2001; 2001US-00892877.
XX
PA (RUBE/) RUBEN S. M.
PA (FLOR/) FLORENCE K. A.

```

RESULT 212
 AA65261
 ID AA65261 standard; DNA; 1447 BP.
 XX
 AC AA65261;
 XX
 DT 23-MAR-2000 (first entry)
 XX
 DB Human secreted protein gene 12.
 XX
 KW Human; secreted protein; cancer; tumour; developmental abnormality;
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
 KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
 KW therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN W0958660-A1.
 XX
 PD 18-NOV-1999.
 XX
 PD 18-NOV-1999.
 XX
 PF 06-MAY-1999; 99WO-US009847.
 XX
 PR 12-MAY-1998; 98US-0085093P.
 PR 12-MAY-1998; 98US-0085094P.
 PR 12-MAY-1998; 98US-0085105P.
 PR 12-MAY-1998; 98US-0085180P.
 PR 18-MAY-1998; 98US-0085906P.
 PR 18-MAY-1998; 98US-0085920P.
 PR 18-MAY-1998; 98US-0085921P.
 PR 18-MAY-1998; 98US-0085922P.
 PR 18-MAY-1998; 98US-0085923P.
 PR 18-MAY-1998; 98US-0085924P.
 PR 18-MAY-1998; 98US-0085925P.
 PR 18-MAY-1998; 98US-0085927P.
 PR 18-MAY-1998; 98US-0085928P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA,
 PI Olesen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR, Lafleur DW,
 PI Andress GA, Edner R;
 XX
 DR WPI; 2000-062296/05.
 DR P-PSDB; AAY76135.
 XX
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders.
 XX
 PS Claim 1; Page 303; 475pp; English.
 XX
 CC AA65250 to AA65350 represent 97 isolated human secreted protein genes.
 CC AA76124 to AA76223 represent the secreted proteins encoded by the 97
 CC human genes. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions, e.g.
 CC by protein or gene therapy. Also pathological conditions can be diagnosed

US-09-989-724-386

Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other

Matches	637;	Conservative	1;	Mismatches	0;	Indels	1;	Gaps	1;
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Db 677 CTGGACATGAAGGAGGCGCATATTAATGATGCCTTCATG 715

XX
DE Human secreted polypeptide cDNA #12.

PA (NIJ/J) NI J.
 PA (ROSE/) ROSEN C A.
 PA (CARTER/) CARTER K C.
 PA (MOORE/) MOORE P A.
 PA (OLSEN/) OLSEN H S.
 PA (SHIT/) SHIT Y.
 PA (YOUNG/) YOUNG B E.
 PA (WEIY/) WEI Y.
 PA (BREWER/) BREWER L A.
 PA (SOPPE/) SOPPE D R.
 PA (LAFLEUR/) LAFLEUR D W.
 PA (ENDR/) ENDRESS B A.
 PA (BIRSE/) BIRSE C B.
 PA (BIRSE/) BIRSE C B.
 PI Ruben SM, Florence KA, NI J, Rosen CA, Carter KC, Moore PA;
 PI Olsen HS, Shi Y, Young PB, Wei Y, Brewer LA, Soppet DR, Lafleur DW;
 PI Endress GA, Ebner R, Birse CB;
 DR WP1; 2003-801210/75
 XX
 XX
 PT New nucleic acid molecule, useful for preparing a medicament for
 PT preventing, treating or ameliorating a medical condition e.g. cancer,
 PT liver disorders or neural disorders.
 XX
 XX
 XX Claim 1; SEQ ID NO 22; 453bp; English.
 XX
 XX The invention relates to human secreted polypeptides and the
 CC polynucleotides encoding them. The sequences are useful for preparing
 CC medicaments for preventing, treating or ameliorating medical conditions
 CC e.g., cancer, liver disorders such as hepatitis or neural disorders such
 CC as Alzheimer's disease. This sequence represents cDNA encoding a human
 CC secreted polypeptide of the invention.
 XX
 XX Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;
 Query Match 98.4%; Score 1324.6; DB 9; Length 1447;
 Best Local Similarity 99.3%; Pred. No. 3.5e-258;
 Matches 1338; Conservative P; Mismatches 6; Indels 1; Gaps 1;

Db 551 GCACTAGCATTTTATTCAGGATCTGGCAAGCTAGAGAAACAAACAAACCTCTGAA 610
 Qy 541 GTGATGAGCGCTGAGATTAAGTGTGAAACATGATCACAATTGAAATGGCATCCCTCT 600
 Db 611 GTGATGAGCGCTGAGATTAAGTGTGAAACATGATCACAATTGAAATGGCATCCCTCT 670
 Qy 601 GATCCCTGAGCATGAGGCGGCGCATTTAAATGATGCTTATGACAGAGATGAGAG 659
 Db 671 GATCCCTGAGCATGAGGCGGCGCATTTAAATGATGCTTATGACAGAGATGAGAG 730
 Qy 660 CTGACCCCTCTGAGAGCGCTGTTTGTGCTTCTGCTGAGAAATTTAAATTTGTTG 719
 Db 731 CTGACCCCTCTGAGAGCGCTGTTTGTGCTTCTGCTGAGAAATTTAAATTTGTTG 790
 Qy 720 TGTGACTGTGAGCATCCGTAATACAGAGCAATCATATATTTGTTGACCATCT 779
 Db 791 TGTGACTGTGAGCATCCGTAATACAGAGCAATCATATATTTGTTGACCATCT 850
 Qy 780 TCTTTTGTATTAATTTTGAATTTGCTTGAAGTGAAGAAAGCAATCATTAACCA 839
 Db 851 TCTTTTGTATTAATTTTGAATTTGCTTGAAGTGAAGAAAGCAATCATTAACCA 910
 Qy 840 CACCACTGAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 899
 Db 911 CACCACTGAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 970
 Qy 900 ATAGGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 959
 Db 971 ATAGGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030
 Qy 960 AAGATCAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1019
 Db 1031 AAGATCAGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1090
 Qy 1020 AGTGAAGATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1079
 Db 1091 AGTGAAGATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1150
 Qy 1080 ACTTATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1139
 Db 1151 ACTTATATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1210
 Qy 1140 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1199
 Db 1211 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1270
 Qy 1200 AGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1259
 Db 1271 AGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1330
 Qy 1260 TTTTCAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1319
 Db 1331 TTTTCAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1390
 Qy 1320 TTTTCAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1346
 Db 1391 TTTTCAATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1417
 RESULT 212
 AAV40540
 ID AAV40540 standard; cDNA; 1401 BP.
 XX
 AC AAV40540;
 XX
 DT 09-NOV-1998 (first entry)
 XX
 DE Homo sapiens secreted protein clone AM42_3.
 XX
 KW Clone; secreted protein; de.
 XX
 OS Homo sapiens.

PT Libraries derived from liver, lung, large intestine, colon, thyroid and
PT pancreas tissue.

PS Example 28; Page 157-158; 398bp; English.

XX AAX40251 to AAX40397 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY11533 to
CC AAY11679, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC present sequence represents a 5' EST from an example of the present
CC invention

SO Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181; Mismatches 0; Indels 1; Gaps 1;
Matches 634; Conservative 4;

```
OY 1 AATGTTGGCTGCTCTTTTCTGAGTGCATTCATGCTGACCTGTCAACAGGT 60
DB 32 AATGTTGGCTGCTCTTTTCTGAGTGCATTCATGCTGACCTGTCAACAGGT 91
OY 61 GCGAAGAAATGCTTTTAAAGTGAACCTTATGATGAGACAGCTCTGGAGATTAAGCAT 120
DB 92 GCGAAGAAATGCTTTTAAAGTGAACCTTATGATGAGACAGCTCTGGAGATTAAGCAT 151
OY 121 GCGTGGATATACCAATGAAATACCTCTTCAAGAGATGAGTCTTCTCATGAGAAA 180
DB 152 GCGTGGATATACCAATGAAATACCTCTTCAAGAGATGAGTCTTCTCATGAGAAA 211
OY 181 GTTCCACAGAGAGACCAAGAAATTTCCATGCTCTTCTCATGATGATACCCAGAG 240
DB 212 GTTCCACAGAGAGACCAAGAAATTTCCATGCTCTTCTCATGATGATACCCAGAG 271
OY 241 GATTCATTCTGTTTGTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTTGAG 300
DB 272 GATTCATTCTGTTTGTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTTGAG 331
OY 301 GTGCATACGACCAATGAAATGAAACAGAGACCGATCAACAGTCTTCTTAAATGAC 360
DB 332 GTGCATACGACCAATGAAATGAAACAGAGACCGATCAACAGTCTTCTTAAATGAC 391
OY 361 CAAACTCTGGAATTTTAAATCCCTTCCACTTGCACACCCATGAGCCCATCTGTG 420
DB 392 CAAACTCTGGAATTTTAAATCCCTTCCACTTGCACACCCATGAGCCCATCTGTG 451
OY 421 CCCATCTGATTTATTAATTTGGTGAATTTTGGATTCATGATGATGATGATGATG 480
DB 452 CCCATCTGATTTATTAATTTGGTGAATTTTGGATTCATGATGATGATGATGATG 511
OY 481 CTGATTTTACAGGATCTGCAACCTGAGAAAGAAAGAAAGAAAGCAATCTGAAGTGA 540
DB 512 CTGATTTTACAGGATCTGCAACCTGAGAAAGAAAGAAAGAAAGCAATCTGAAGTGA 571
OY 541 GACGCTGAAGATTAAGTGAAGAAACATGATCAATGTAAGATGAGCATCCCTCTGATCC 600
DB 572 GACGCTGAAGATTAAGTGAAGAAACATGATCAATGTAAGATGAGCATCCCTCTGATCC 631
OY 601 CTGAGCATGAGGGG-GGGCATATTATGATGAGCCCTGATG 638
DB 632 CTGAGCATGAGGGG-GGGCATATTATGATGAGCCCTGATG 670
```

DB 632 CTGAGCATGAGGGG-GGGCATATTATGATGAGCCCTGATG 670

RESULT 217

ID AAX39430

AXX39430; standard; DNA; 848 BP.

21-JUN-1999 (first entry)

Human secreted protein 5' EST SEQ ID NO: 27.

Human; secreted protein; EST; expressed sequence tag; diagnosis;

Forensic; gene therapy; chromosome mapping; signal peptide;

upstream regulatory sequence; cytokine activity; cell proliferation;

differentiation; haematopoiesis regulation; tissue growth regulation;

reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;

thrombolytic; anti-inflammatory; tumour inhibition; ds.

Homo sapiens.

MO9906551-A2.

11-FEB-1999.

31-JUL-1998; 98MO-1B001235.

01-ANG-1997; 97US-00905133.

(BEST) GENSET.

Dumas Mline Edwards J, Duclert A, Lacroix B;

WPI; 1999-153781/13.

P-PSDB; AAM93620, AAY11373.

New nucleic acids encoding human secreted - proteins obtained from cDNA

libraries prepared from substantia nigra, cerebellum, adrenals and fetal

brain tissue.

Example 28; Page 157-158; 434bp; English.

AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for

human secreted proteins, and encode the proteins given in AAY11374 to

AAY11531, respectively. The proteins given represent the signal peptide

and an N-terminal fragment of a secreted protein. The nucleic acid

sequences can be used for producing secreted human gene products. They

can also be used to develop products for diagnosis and therapy. The

proteins obtained may have cytokine activity, cell

proliferation/differentiation activity, haematopoiesis regulating

activity, tissue growth regulating activity, reproductive hormone

regulating activity, chemotactic/chemokinetic activity, haemostatic and

thrombolytic activity, receptor/ligand activity, anti-inflammatory

activity, tumour inhibition activity or other activities. The products

can be used in forensic, gene therapy and chromosome mapping procedures.

The sequences can also be used for obtaining corresponding promoter

sequences. The nucleic acids encoding the signal peptide can be used for

directing extracellular secretion of a polypeptide or the insertion of a

polypeptide into a membrane, or importing a polypeptide into a cell. This

sequence encodes the human 5' EST secreted proteins represented in

AAM93620 and AAY11373

Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181; Mismatches 0; Indels 1; Gaps 1;

Matches 634; Conservative 4;

```
OY 1 AATGTTGGCTGCTCTTTTCTGAGTGCATTCATGCTGACCTGTCAACAGGT 60
DB 32 AATGTTGGCTGCTCTTTTCTGAGTGCATTCATGCTGACCTGTCAACAGGT 91
```

QY 541 GACCTGAGATTAAGTGTGAAACATGATCAATTTGAAATGGCATCCCTGTGATCCC 600
DB 572 GACCTGAGATTAAGTGTGAAACATGATCAATTTGAAATGGCATCCCTGTGATCCC 631
QY 601 CTGACATGAAAGG-GGGCATTTAATGATGCTTCATG 638
DB 632 CTGACATGAAAGGAGGGCATTTAATGATGCTTCATG 670

RESULT 2
US-09-247-155-27
Sequence 27, Application US/09247155A
Patent No. 6312922

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Aymeric
APPLICANT: Bouqueloret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/247,155A
EARLIER FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 27
LENGTH: 848
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 32..73
OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTTGAGCTGCTCTTTTCTGAGTCTGCATTCATGCTGAAGCTCTGTCAACAGGT 60
DB 32 ATGTTGAGCTGCTCTTTTCTGAGTCTGCATTCATGCTGAAGCTCTGTCAACAGGT 91
QY 61 GCAGAAATGCTTTTAAAGTGAAGTATGATCAAGACGCTGGAGATTAAGCATAT 120
DB 92 GCAGAAATGCTTTTAAAGTGAAGTATGATCAAGACGCTGGAGATTAAGCATAT 151
QY 121 GCCGGGATTCATATGAAGTATCTCTCAAGAGATGTAAGTTCTCATAGAGAAA 180
DB 152 GCCGGGATTCATATGAAGTATCTCTCAAGAGATGTAAGTTCTCATAGAGAAA 211
QY 181 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTCAATTTGCAATGTAACCAAGG 240
DB 212 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTCAATTTGCAATGTAACCAAGG 271
QY 241 GTATCATTTGTTTGTGTTAAGACCTTCATCAAAAATCAACCTTCTGCTGTGAG 300
DB 272 GTATCATTTGTTTGTGTTAAGACCTTCATCAAAAATCAACCTTCTGCTGTGAG 331
QY 301 GTGCAATGAGGCAATGAAGTGAAGACAGCATCAAGTCTGCTTTCTTAATGAC 360
DB 332 GTGCAATGAGGCAATGAAGTGAAGACAGCATCAAGTCTGCTTTCTTAATGAC 391
QY 361 CAAACTCTGAAATTTTAAATATCCCTTCAACATTCGACCAACCAAGGACCAATCTG 420
DB 392 CAAACTCTGAAATTTTAAATATCCCTTCAACATTCGACCAACCAAGGACCAATCTG 451

QY 421 CCATCTGATTAATTAATTTGTTGATATTTTGCATCATGATGATGCAATGCACTA 480
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QY 481 CTGATTTTCAAGGATCTGCAACCTGAGAAAGAAACAAAGAACCATCTGAAGTGAT 540
DB 512 CTGATTTTCAAGGATCTGCAACCTGAGAAAGAAACAAAGAACCATCTGAAGTGAT 571
QY 541 GACCTGAGATTAAGTGTGAAACATGATCAATTTGAAATGGCATCCCTGTGATCCC 600
DB 572 GACCTGAGATTAAGTGTGAAACATGATCAATTTGAAATGGCATCCCTGTGATCCC 631
QY 601 CTGACATGAAAGG-GGGCATTTAATGATGCTTCATG 638
DB 632 CTGACATGAAAGGAGGGCATTTAATGATGCTTCATG 670

RESULT 3
US-09-663-600A-27

Sequence 27, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Aymeric
APPLICANT: Bouqueloret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.053.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
EARLIER FILING DATE: 2000-09-15
EARLIER APPLICATION NUMBER: 09/191,997
EARLIER FILING DATE: 1998-11-13
EARLIER APPLICATION NUMBER: 60/066,677
EARLIER FILING DATE: 1997-11-13
EARLIER APPLICATION NUMBER: 60/069,957
EARLIER FILING DATE: 1997-12-17
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 27
LENGTH: 848
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 32..73
OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 121 GCCGGGATTCATATGAAGTATCTCTCAAGAGATGTAAGTTCTCATAGAGAAA 180
DB 152 GCCGGGATTCATATGAAGTATCTCTCAAGAGATGTAAGTTCTCATAGAGAAA 211
QY 181 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTCAATTTGCAATGTAACCAAGG 240

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Post-processing: Minimum Match 80%

Maximum Match 100%

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Listing first 65000 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1346	100.0	1346	6 AR252633	AR252633 Sequence
2	1346	100.0	1346	6 AX403499	AX403499 Sequence
3	1346	100.0	1346	6 AX464348	AX464348 Sequence
4	1346	100.0	1346	6 AY359060	AY359060 Homo sapi
5	1328.6	98.7	1605	9 BC014317	BC014317 Homo sapi
6	1325.4	98.5	1377	9 BC050606	BC050606 Homo sapi
7	1325.4	98.5	1440	9 BC015099	BC015099 Homo sapi
8	1324.6	98.4	1447	6 BD205644	BD205644 97 human
9	1321.8	98.2	1401	6 BD083420	BD083420 Secreted
10	1309.4	97.3	1347	6 AX083392	AX083392 Sequence
11	1307.8	97.2	1345	9 AF229179	AF229179 Homo sapi
12	1305	97.0	1356	6 BD135300	BD135300 110 human

ALIGNMENTS

RESULT 1
LOCUS AR252633 1346 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 386 from patent US 6478825.
ACCESSION AR252633
VERSION AR252633.1 GI:27300541
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kees,D.
TITL Implant, method of making same and use of the implant for the
treatment of bone defects
JOURNAL Patent: US 6478825-A 386 12-NOV-2002;
FEATURES
Location/Qualifiers
source 1..1346
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
AX403499 1346 bp DNA linear PAT 14-JUN-2002
LOCUS

DEFINITION Sequence 386 from Patent WO0073454.
AX403499
VERSION AX403499.1 GI:21436987
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 Ashkenazi, A.J., Baker, K.P., Bolstein, D., Desnoyers, L., Batou, D.,
Perrera, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Guiney, A.L., Kijavlin, I., Napier, M.A., Pan, J.,
Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0073454-A 386 07-DEC-2000;
Genentech Inc. (US)
FEATURES
source
1. 1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 1346; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	841	ACCACTGAATCATTAAGTATTTACAGACTCAAAATATCTTAATATTTTCTGACAGTA	900
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Dp	901	TAGATATTAATATGTGTCATGTGTAATTTGTAGTATATTAATTAAGCATTTTGAATA	960
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Dp	1021	GTGAGAAATACATATATATATGTGTGTAAGAAATCATTTGAAATAGATCCTTTTGACATCA	1080
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Qy	1141	TGGAATAAAAATGGAATTACTCATATACAGGGTGAATTTTATCTGTATGACACACA	1200
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DEFINITION	Sequence 481 from Patent WO0140466.	linear	PAT 16-JUN-2002
ACCESSION	AX464348		
VERSION	AX464348.1	GI:21899190	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
	Homo sapiens		
	Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Pilvaroff, E.,		
	Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gunney, A.L.,		
	Shenwood, S., Smith, V., Stewart, T.A., Tunas, D., Watanabe, C.K.,		
	Wood, W.L. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
	same		
JOURNAL	Patent: WO 0140466-A 481 07-JUN-2001;		
FEATURES	Genentech Inc. (US)		
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RESULT 4
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LOCUS Homo sapiens clone DNA61873 NX-17 (UN0678) mRNA, complete cds.
DEFINITION AY359060
ACCESSION AY359060.1 GI:37183237
VERSION
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1346)
Clark,H.F., Gurney,A.L., Abaya,B., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Denel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hase,P.B.,
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,R., Sanchez,C.,
Schenfeld,J., Seebagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vamliem,R., Watanabe,C., Wleand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)

JOURNAL
PUBMED 12975309
2 (bases 1 to 1346)
REFERENCE Clark,H.F.
AUTHORS Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

FEATURES
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ORIGIN
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2e-266;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 961 AGATCAGCATATGATATATATTTTCACTTCAAGACCTAAGGAAAAATATATTTTCCA 1020
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 DB 1321 AAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 5
 LOCUS BC014317 1605 bp mRNA linear PRI 04-OCT-2003
 DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
 WGC:22707 IMAGE:4048217), complete cds.
 ACCESSION BC014317
 VERSION BC014317.1 GI:15680012
 KEYWORDS MGC.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1605)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derg, J.G.,
 Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheer, T.E., Brownstein, M.J., Umedin, T.B., Toshiki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hui, S.W.,
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Sanchez, J., Holton, E., Kettelman, M., Madan, A., Young, A.C., Scherchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
 Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmitt, J., Myers, R.M.,
 Butcherfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 12477932
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 2 (bases 1 to 1605)
 Strausberg, R.
 Direct Submission
 Submitted (17-SEP-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK

COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
 Contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahney, Erin Helton, Mark Kettelman, Anuradha
 Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 31 Row: n Column: 3.
 Location/Qualifiers

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source

gene

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ORIGIN

Query Match 98.7%; Score 1328.6; DB 9; Length 1605;
 Best Local Similarity 99.6%; Pred. No. 7,5e-263;
 Matches 1342; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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RESULT 6
 BC050606 1377 bp mRNA linear PRI 12-NOV-2003
 LOCUS Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
 DEFINITION MGC:60059 IMAGE:5183554), complete cds.
 ACCESSION BC050606
 VERSION BC050606.1 GI:30047080

KEYWORDS

MGC.
Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1377)

AUTHORS

Strausberg, R.L., Pelngold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P.,
Diatchenko, L., Marisano, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Cabavati, T.L.,
Schaefer, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abrams, R.D., Mullaly, S.J., Bosak, S.A., McKean, P.J.,
McKernan, K.J., Malek, J.A., Gnaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahney, J., Heltion, B., Kettman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywicki, M.I., Skalek, U., Smallegange, D.B.,
Schmerch, A., Schein, J.B., Jones, S.J., and Marz, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE

JOURNAL
MEDLINE
PUBMED
22388257
12477932
2 (bases 1 to 1377)
Strausberg, R.
Direct Submission
Submitted (08-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (ILNI)
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.sbgp.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

REMARK

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNI at: <http://image.llnl.gov>
Series: IRAP Plate: 110 Row: c Column: 4
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FEATURES

source
gene

CDS

BC050606 1377 bp mRNA linear PRI 12-NOV-2003
LOCUS Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
DEFINITION MGC:60059 IMAGE:5183554), complete cds.
ACCESSION BC050606
VERSION BC050606.1 GI:30047080

REMARK
COMMENT

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
 Contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahey, Erin Heltton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRL Plate: 31 Row: d Column: 11.
 Location/Qualifiers

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CDS

ORIGIN

Query Match 98.5%; Score 1325.4; DB 9; Length 1440;
 Best Local Similarity 99.5%; Pred. No. 3.4e-262; Indels 1; Gaps 1;
 Matches 1340; Conservative 0; Mismatches 6;

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 61 CCAAGTGCAAAATGCTTTAAAGTGAAGTATGATGCAACAGCTTGGAGATAA 120
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RESULT 8
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 LOCUS 1447 bp DNA linear PAT 17-JUL-2003
 DEFINITION 97 human secreted proteins.
 ACCESSION BD205644

VERSION	BD05644.1	GI:33015414
KEYWORDS	JP 2002533058-A/21.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Ruben,S.M., Florence,K., Ni,U., Rosen,C.A., Carter,K.C., Moore,P.A., Olsen,R.S., Shi,Y., Young,P.B., Wei,F.P., Brewer,L.A., Soppel,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.R.	
TITLE	97 human secreted proteins	
JOURNAL	Patent: JP 2002533058-A 21 08-Oct-2002;	
COMMENT	HUMAN GENOME SCIENCES INC OS Homo sapiens (human) JP 2002533058-A/21	
PD	08-OCT-2002	
PF	06-MAY-1999 JP 2000548451	
PR	12-MAY-1998 US 60/085093,12-MAY-1998 US 60/085180 PR	
12-MAY-1998 US	60/085105,12-MAY-1998 US	60/085094 PR
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18-MAY-1998 US	60/085924,18-MAY-1998 US	60/085906 PR
18-MAY-1998 US	60/085923,18-MAY-1998 US	60/085922 PR
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18-MAY-1998 US	60/085920	60/085928 PR
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PI	C CARTER,	
PI	PAUL A MOORE,HENRIK S OLSEN,YANGU SHI,PAUL B YOUNG,PING FBI	
PI	WEI,	
PI	LAURIE A BREMER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A PI	
ENDRESS,		
PI	REINHARD EBNER	
PC	C12N1/21,	
PC	C12N5/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC	
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PC	C12N5/10,C12P21/02,C12N15/00,C12N5/00	
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PH	Key	Location/Qualifiers
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DEFINITION Secreted protein and polynucleotides encoding them.
ACCESSION BD083420
VERSION BD083420.1 GI:22629030
KEYWORDS JP 2001523950-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1401)
AUTHORS Jacobs, K., McCoy, J.M., Lavallie, R.R., Racie, L.A., Merberg, D.,
Trecy, M., Spaulding, V. and Agostino, M.J.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2001523950-A 2 27-NOV-2001,
GENETICS INSTITUTE INC
COMMENT PN JP 2001523950-A/2
PD 27-NOV-2001
PF 23-JAN-1998 JP 1998532177
PR 24-JAN-1997 US 08/788789
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIB, PI
DAVID MERBERG,
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:
Double;
CC Topology: Linear;
FH Key Location/Qualifiers.
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Best Local Similarity 99.8%; Pred. No. 1, 9e-261;
Matches 1334; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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DEPOSITION Sequence 84 from Patent WO0112660.
ACCESSION AX083392
VERSION AX083392.1 GI:13185232
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kato, S. and Kimura, T.
TITLE Human proteins having hydrophobic domains and dnas encoding these proteins
JOURNAL Patent: WO 0112660-A 84 22-FEB-2001;
SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)
FEATURES Location/Qualifiers

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Query Match 97.3%; Score 1309.4; DB 6; Length 1347;
Best Local Similarity 99.8%; Pred. No. 6.8e-259;
Matches 1321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DEFINITION AF229179
ACCESSION AF229179.1 GI:9957753
VERSION AF229179.1 GI:9957753
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Zhang,H., Wada,J., Hida,K., Tsuchiyaama,Y., Hiragushi,K., Shikata,K., Wang,H., Iin,S., Kanwar,Y.S. and Makino,H.
TITLE Collectrin, a collecting duct-specific transmembrane glycoprotein, is a novel homolog of ACE2 and is developmentally regulated in embryonic kidneys
JOURNAL J. Biol. Chem. 276 (20), 17132-17139 (2001)
MEDLINE 21264468
PUBMED 11278314
REFERENCE
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Human kidney specific membrane protein (NX-17)
JOURNAL Unpublished
AUTHORS Zhang,H., Wada,J. and Makino,H.
TITLE Direct Submission
JOURNAL Submitted (28-JAN-2000) Department of Medicine III, Okayama University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558, Japan

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Best Local Similarity 99.8%; Pred. No. 1,4e-258;
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RESULT 12
BD135300
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITL
JOURNAL
COMMENT

BD135300 1356 bp DNA linear PAT 18-SEP-2002
110 human secretory proteins.
BD135300.1 GI:23230245
JP 2002508167-A/51.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1356)
Moore,P.A., Ruben,S.M., Carter,K.C., Shi,Y., Rosen,C.A., Soppet,D.R., Caou,H., Wei,Y.P., Florence,K., Duan,R.D., Florence,C., Greene,J.M., Peng,P., Ferrie,A.M., Yu,G.L., Janat,F. and N.Y.
110 human secretory proteins
Patent: JP 2002508167-A 51 19-MAR-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002508167-A/51
PD 19-MAR-2002
PP 17-DEC-1998 JP 2000539040
PR 18-DEC-1997 US 60/070 923,18-DEC-1997 US 60/068 007 PR
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18-DEC-1997 US 60/068 008,18-DEC-1997 US 60/068 054 PR
18-DEC-1997 US 60/068 064,18-DEC-1997 US 60/068 053 PR
19-DEC-1997 US 60/068 167,19-DEC-1997 US 60/068 368 PR
19-DEC-1997 US 60/068 369,19-DEC-1997 US 60/068 369 PR
19-DEC-1997 US 60/068 365

PI PAUL A MOORE, STEVEN M RUBEN, KENNETH C CARTER, YANGU SHI, CRAIG
PI A ROSEN,
PI DANIEL R SOPPRT, HARA CAU, YING FEI WEI, KIMBERLY FLORENCE, PI
ROSANNE D DUAN,
PI CHARLES FLORENCE, JOHN M GREENE, PING FENG, ANN M FERRIE, GUO PI
LIANG YU,
PI FORJ JANAT, JIAN NI
PC C12N15/09, A6IK38/00, A6IK48/00, A6IP9/00, A6IP9/10, A6IP15/00, PC
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PC A6IP29/00, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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A6IK37/02,
PC C12N5/00
CC n equals a, c, g, or c
FH Key Location/Qualifiers
FT source 1.1356 Location/Qualifiers
FEATURES
source Location/Qualifiers
1.1356
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 97.0%; Score 1305; DB 6; Length 1356;
Best Local Similarity 99.0%; Pred. No. 5.4e-258;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

1 GAAAGATGTTTGGCTCTCTTTTCTGAGACGCTCATTCAGTGGAGACTGTGCA 60
12 GAAAGATGTTTGGCTCTCTTTTCTGAGACGCTCATTCAGTGGAGACTGTGCA 71
61 CCAAGTCCAGAAATGCTTTAAAGTGAAGTATGATCAGAAACGCTCTGGAGATAA 120
72 CCAAGTCCAGAAATGCTTTAAAGTGAAGTATGATCAGAAACGCTCTGGAGATAA 131
121 GCATATGCTCTGGATACCAATGAAGAAATGCTTTCAAGGAGATGCTTTCTCAATG 180
132 GCATATGCTCTGGATACCAATGAAGAAATGCTTTCAAGGAGATGCTTTCTCAATG 191
181 AGAAAGTCTCCCAAGAGAGCAAGAAATTTCCCATGCTTCTTGAATGAAC 240
192 AGAAAGTCTCCCAAGAGAGCAAGAAATTTCCCATGCTTCTTGAATGAAC 251
241 CAGAGGATCATCTGCTTTGCTGATCAGACCTTCAAAAATCAGACCTTCTGCT 300
252 CAGA-GGATATCTGCTTTGCTGATCAGACCTTCAAAAATCAGACCTTCTGCT 310
301 GTTGAAGTGCATGACCCATGAAGATGAACAAACCGGATCAACATGCTTTCTTCTA 360
311 GTTGAAGTGCATGACCCATGAAGATGAACAAACCGGATCAACATGCTTTCTTCTA 370
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431 TCTGTCCTCATCTGATATTAATTTGCTGATATTTTGCATCATATGTTGCAATT 490
481 GCACCTACTGATTTTATCAGGATCTGCAACGTAGAGAAAGAAACCAATCTGA 540
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Search completed: June 6, 2004, 13:05:18
Job time : 5280.77 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: June 6, 2004, 07:26:44 ; Search time 544.777 Seconds
(without alignments)
10496.171 Million cell updates/sec

Title: US-09-989-724-386

Perfect score: 1346
Sequence: 1 gaagaagatcgtcgtcgtc.....aaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues
Total number of hits satisfying chosen parameters: 220

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

Database : N_Geneseq_29Jan04:*

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- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001bs:*
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- 7: geneseqn2003as:*
- 8: geneseqn2003bs:*
- 9: geneseqn2003cs:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1346	100.0	1346	4	AAS21484 Human CDN
5	1346	100.0	1346	5	AAE44243 Human PRO
6	1346	100.0	1346	5	ABX77959 Human PRO
7	1346	100.0	1346	7	ABX80371 Human PRO
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9	1346	100.0	1346	7	ACD24093 Human CDN
10	1346	100.0	1346	7	ABX90348 Human sec
11	1346	100.0	1346	7	ABX64194 Human sec
12	1346	100.0	1346	7	ACB67234 Human enco
13	1346	100.0	1346	7	ACA64416 Human hum
14	1346	100.0	1346	7	ACA03843 Human enco
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16	1346	100.0	1346	7	ABX80875 Human sec
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21	1346	100.0	1346	7	ABX81258 Human hum
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23	1346	100.0	1346	7	ACA93074 Human hum

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124	1346	100.0	1346	9	ADC50522	Novel	hum
125	1346	100.0	1346	9	ADC72089	Novel	hum
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128	1346	100.0	1346	9	ADC57409	Novel	hum
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210	1324.6	98.4	1447	3	ADA65261	Human	sec
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213	1309.4	97.3	1347	4	AAV94470	Human	hyd
214	1307.8	97.2	1345	7	ABZ78127	Human	can
215	1307.4	97.1	1365	4	AAH98224	Human	EST
216	1305	97.0	1356	2	AAV97957	Human	sec
217	1305	97.0	1356	7	ADA56545	Gene	encc
218	1305	97.0	1356	7	ADA40381	Human	sec
219	1305	97.0	1356	8	ADA11594	Human	CDN
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ALIGNMENTS

RESULT 1	
ID	AAZ65097 strand; cDNA; 1346 BP.
AAZ65097;	
AC	05-APR-2000 (first entry)
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XX	Membrane-bound protein PRO1312 encoding cDNA.
XX	
XX	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
KW	pharmacological; receptor immunoadhesin; gene mapping; ss.
XX	
XX	Homo sapiens.
OS	
XX	
PN	WO9963088-A2.
XX	

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Db 1201 GTTGATATATATTTTCTGATATACAGCCCTTAATAGCAATTTGTTGACCAT 1260
Qy 1261 TCTACATTTTGTAAAGTCCATCTGCTACTTAATTAATTAATCACTCTTTT 1320
Db 1261 TCTACATTTTGTAAAGTCCATCTGCTACTTAATTAATTAATCACTCTTTT 1320
Qy 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
Db 1321 AAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 203

ADE89344 ID ADE89344 standard; cDNA; 1346 BP.

XX AC ADE89344;

XX DT 29-JAN-2004 (first entry)

XX DE Human PRO polynucleotide #241.

KM Human; Gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor- α ; TNF- α ; chondrocyte cell; tumour;
cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
liver; microvascular endothelial cell; glucose; FFA;
skeletal muscle cell; adipocyte cell; pericyte cell;
inner ear utricular supporting cell; T-lymphocyte cell;
endothelial cell tube formation; bone disorder; cartilage disorder;
sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
rheumatoid arthritis; haemoglobin-associated disorder thalassaemia;
immune system cell infiltration.

XX Homo sapiens.

XX OS US2003199062-A1.

XX PD 23-OCT-2003.

XX PF 17-APR-2002; 2002US-00124823.

XX 31-MAR-1997; 97MO-US005230.
PR 12-JUN-1998; 98MO-US012456.
PR 14-JUL-1998; 98MO-US014552.
PR 28-AUG-1998; 98MO-US017888.
PR 10-SEP-1998; 98MO-US018824.
PR 14-SEP-1998; 98MO-US019093.
PR 14-SEP-1998; 98MO-US019094.
PR 14-SEP-1998; 98MO-US019177.
PR 16-SEP-1998; 98MO-US019330.
PR 17-SEP-1998; 98MO-US019437.
PR 07-OCT-1998; 98MO-US021141.
PR 29-OCT-1998; 98MO-US022991.

PR 29-OCT-1998; 98MO-US022992.
PR 20-NOV-1998; 98MO-US024855.
PR 01-DEC-1998; 98MO-US025108.
PR 05-JAN-1999; 99MO-US000106.
PR 08-MAR-1999; 99MO-US005028.
PR 10-MAR-1999; 99MO-US005190.
PR 20-APR-1999; 2000MO-US006319.
PR 14-MAY-1999; 99MO-US008615.
PR 02-JUN-1999; 99MO-US010733.
PR 01-SEP-1999; 99MO-US012252.
PR 08-SEP-1999; 99MO-US020111.
PR 13-SEP-1999; 99MO-US020594.
PR 15-SEP-1999; 99MO-US020944.
PR 05-OCT-1999; 99MO-US021090.
PR 29-NOV-1999; 99MO-US021547.
PR 30-NOV-1999; 99MO-US028301.
PR 01-DEC-1999; 99MO-US028301.
PR 02-DEC-1999; 99MO-US028511.
PR 02-DEC-1999; 99MO-US028551.
PR 16-DEC-1999; 99MO-US028565.
PR 20-DEC-1999; 99MO-US030095.
PR 20-DEC-1999; 99MO-US030911.
PR 22-DEC-1999; 99MO-US030999.
PR 30-DEC-1999; 99MO-US031243.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000277.
PR 11-FEB-2000; 2000MO-US000376.
PR 18-FEB-2000; 2000MO-US003565.
PR 22-FEB-2000; 2000MO-US004341.
PR 24-FEB-2000; 2000MO-US004342.
PR 24-FEB-2000; 2000MO-US004914.
PR 01-MAR-2000; 2000MO-US005004.
PR 02-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005746.
PR 15-MAR-2000; 2000MO-US005841.
PR 20-MAR-2000; 2000MO-US006884.
PR 21-MAR-2000; 2000MO-US007377.
PR 30-MAR-2000; 2000MO-US007532.
PR 17-MAY-2000; 2000MO-US008439.
PR 22-MAY-2000; 2000MO-US013705.
PR 30-MAY-2000; 2000MO-US014042.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001MO-US006520.
PR 01-MAR-2001; 2001MO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001US-00872035.

PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
PX (GETH) GENENTECH INC.
PA
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W,
PI Gerltsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S,
PI Smith V, Stewart TA, Tumas D, Matanabe CK, Wood WI, Zhang Z;
XX WPI; 2004-041360/04.
DR P-PSDB; ADE89345.
XX
PT Novel isolated PRO polypeptide useful for treating diabetes, hyper- or
PT hypo-insulinemia, sports injuries, arthritis, obesity, stroke, heart
PT attack, various coagulation disorders, tumors.
XX
XX Claim 2; SEQ ID NO 481; 638pp; English.
XX
XX The invention relates to isolated human PRO polypeptides (secreted and
XX transmembrane polypeptides) and the polynucleotides encoding them. The
XX invention also relates to an antibody which specifically binds to a PRO
XX polypeptide, a method for stimulating the release of tumor necrosis
XX factor-alpha (TNF-alpha) from human blood, a method for stimulating the
XX proliferation or differentiation of chondrocyte cells and a method for
XX detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
XX colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
XX polynucleotides are useful in molecular biology, including uses as
XX hybridisation probes, in chromosome and gene mapping, in generating
XX antisense RNA and DNA and in gene therapy. The polynucleotides may also
XX be used in preparing PRO polypeptides by recombinant techniques and in
XX generating either transgenic animals or knock-out animals which are
XX useful in the development and screening of therapeutically useful
XX reagents. The PRO polypeptides or antibodies are used in preparing a
XX medicament for treating a condition responsive to the polypeptides or
XX antibodies, such as tumours, for stimulating and inhibiting proliferation
XX of human microvascular endothelial cells, for modulating the uptake of
XX glucose or PPA by skeletal muscle cells or adipocyte cells, for
XX stimulating differentiation of adipocyte cells, for stimulating
XX proliferation of or gene expression in pericyte cells, for stimulating
XX the proliferation of inner ear utricular supporting cells or T-lymphocyte
XX cells, for inducing endothelial cell tube formation and for treating
XX various bone and/or cartilage disorders such as sports injuries and
XX arthritis. PRO polypeptides which stimulate the release of proteoglycans
XX from cartilage are useful for treating sports-related joint problems.
XX articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
XX polypeptides are also useful for treating various mammalian haemoglobin-
XX associated disorders such as various thalassemias and conditions which
XX may benefit from enhanced local immune system cell infiltration. This
XX sequence represents a human PRO polynucleotide of the invention. Note:
XX The sequence data for this patent is also available in electronic format
XX from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 1346; DB 10; Length 1346;
XX Best Local Similarity 100.0%; Pred. No. 1.6e-262;
XX Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 CCAAGTGCAGAAATGCTTTTAACTGAGACTTATGATCAGAACAGCTCTGGAGATTA 120
DB 61 CCAAGTGCAGAAATGCTTTTAACTGAGACTTATGATCAGAACAGCTCTGGAGATTA 120
QY 121 GCATATGCTGGGATACCAATGAGAAATACCTCTTCAAGCAGTGTAGCTTTCTCCAG 180
DB 121 GCATATGCTGGGATACCAATGAGAAATACCTCTTCAAGCAGTGTAGCTTTCTCCAG 180
QY 161 AGAAAGTTCCTCCAGAGAGCAAGAAATTTCCATGTCCTACTTGCAATGTAAC 240
DB 161 AGAAAGTTCCTCCAGAGAGCAAGAAATTTCCATGTCCTACTTGCAATGTAAC 240
QY 241 CAGAGGATACATTCCTGTTTGTGTTTCAAGACCTTCAAAAATACACCCCTCTGCT 300
DB 241 CAGAGGATACATTCCTGTTTGTGTTTCAAGACCTTCAAAAATACACCCCTCTGCT 300
QY 301 GTTGAAGTGCATACGACCAATGAAATGAAACAAAGAACCGATCAAAATGCTTTCTA 360
DB 301 GTTGAAGTGCATACGACCAATGAAATGAAACAAAGAACCGATCAAAATGCTTTCTA 360
QY 361 AATGACCAAACTCTGAAATTTTAAATCCCTGCACCTTGACACCCATGAGACCA 420
DB 361 AATGACCAAACTCTGAAATTTTAAATCCCTGCACCTTGACACCCATGAGACCA 420
QY 421 TCTGTGCCCATCTGATTAATATTTGGTGTGATATTTTGATCATCATGTGCAATT 480
DB 421 TCTGTGCCCATCTGATTAATATTTGGTGTGATATTTTGATCATCATGTGCAATT 480
QY 481 GCACTACTGATTTTATCAGGGATCTGCGACCTAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 GCACTACTGATTTTATCAGGGATCTGCGACCTAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GTGATGACGCTGAAAGATTAAGTGAAGAAACATGATCAATTTGAAATGCGATCCCTCT 600
DB 541 GTGATGACGCTGAAAGATTAAGTGAAGAAACATGATCAATTTGAAATGCGATCCCTCT 600
QY 601 GATCCCTCTGACATGAAAGGGGGCATATTAATGATGCTTCATGACAGAGATGAGAGC 660
DB 601 GATCCCTCTGACATGAAAGGGGGCATATTAATGATGCTTCATGACAGAGATGAGAGC 660
QY 661 TCAACCTCTCTGAAAGGGCTGTGTTGCTCTCCCAAGAAATTTAACTTTGTTCTCT 720
DB 661 TCAACCTCTCTGAAAGGGCTGTGTTGCTCTCCCAAGAAATTTAACTTTGTTCTCT 720
QY 721 GTGATGCTGACATCTGAAATACCAAGAGAGATCATATTTGTTCAACATTTCT 780
DB 721 GTGATGCTGACATCTGAAATACCAAGAGAGATCATATTTGTTCAACATTTCT 780
QY 781 CTTTGTATTAATTTTGAATGTGCTTGAAGTGAAGAGATCAATTTTACCACCAAC 840
DB 781 CTTTGTATTAATTTTGAATGTGCTTGAAGTGAAGAGATCAATTTTACCACCAAC 840
QY 841 ACCACTGAATATTAAGCTATTCACAGATCAAAATTTCTAATTAATTTTCTGACAGTA 900
DB 841 ACCACTGAATATTAAGCTATTCACAGATCAAAATTTCTAATTAATTTTCTGACAGTA 900
QY 901 TAGGTATTAATGAGTCAATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 960
DB 901 TAGGTATTAATGAGTCAATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTT 960
QY 961 AGATGAGGATATGATTAATTTTCACTTCAAAAGCTTAAGAGAGAGAGAGAGAGAGAG 1020
DB 961 AGATGAGGATATGATTAATTTTCACTTCAAAAGCTTAAGAGAGAGAGAGAGAGAGAG 1020
QY 1021 GTGAGGATATCATTAATGATGATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB 1021 GTGAGGATATCATTAATGATGATGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY 1081 CTTATATCACTCTGATATGATTAAGTAAACAAAGAGTGAAGTATTAATTTAAATGGA 1140
DB 1081 CTTATATCACTCTGATATGATTAAGTAAACAAAGAGTGAAGTATTAATTTAAATGGA 1140

QY 1141 TGGATATAATGAAATTAATCATATACAGGTGAGATTTTATCTGTATACACCAACA 1200
DB 1141 TGGATATAATGAAATTAATCATATACAGGTGAGATTTTATCTGTATACACCAACA 1200
QY 1201 GTTGATATATATTTTCTGAATATACAGCCCTTAATAGACAATTTGTTGACCAAT 1260
DB 1201 GTTGATATATATTTTCTGAATATACAGCCCTTAATAGACAATTTGTTGACCAAT 1260
QY 1261 TCTACATTTTGTAAAGTCCAAATCTGTGCTAACTTAATTAAGTAATATCATCTCTTTT 1320
DB 1261 TCTACATTTTGTAAAGTCCAAATCTGTGCTAACTTAATTAAGTAATATCATCTCTTTT 1320
QY 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
DB 1321 AAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 204
ADE18483
ID ADE18483 standard; cDNA; 1346 BP.
AC ADE18483;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human PRO polynucleotide #241.
XX
KW Human; gene; b6; PRO; secreted polypeptide; transmembrane polypeptide;
KW tumour necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
KW cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
KW liver; microvascular endothelial cell; glucose; FFA;
KW skeletal muscle cell; adipocyte cell; pericyte cell;
KW inner ear utricle supporting cell; T-lymphocyte cell;
KW endothelial cell tube formation; bone disorder; cartilage disorder;
KW sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
KW rheumatoid arthritis; haemoglobin-associated disorder thalassemia;
KW immune system cell infiltration.
XX
OS Homo sapiens.
XX
PN US2003194794-A1.
XX
PD 16-OCT-2003.
XX
PF 17-APR-2002; 2002US-00125805.
XX
PR 31-MAR-1997; 97MO-US005230.
PR 12-JUN-1998; 98MO-US012456.
PR 14-JUL-1998; 98MO-US014552.
PR 28-AUG-1998; 98MO-US017888.
PR 10-SEP-1998; 98MO-US018824.
PR 14-SEP-1998; 98MO-US019093.
PR 14-SEP-1998; 98MO-US019094.
PR 16-SEP-1998; 98MO-US019330.
PR 17-SEP-1998; 98MO-US019437.
PR 07-OCT-1998; 98MO-US021141.
PR 29-OCT-1998; 98MO-US022991.
PR 29-OCT-1998; 98MO-US022992.
PR 20-NOV-1998; 98MO-US024855.
PR 01-DEC-1998; 98MO-US025108.
PR 05-JAN-1999; 99MO-US000106.
PR 08-MAR-1999; 99MO-US005028.
PR 10-MAR-1999; 99MO-US005190.
PR 10-MAR-1999; 2000MO-US006319.
PR 20-APR-1999; 99MO-US008615.
PR 14-MAY-1999; 99MO-US010733.
PR 02-JUN-1999; 99MO-US012252.
PR 01-SEP-1999; 99MO-US020111.
PR 08-SEP-1999; 99MO-US020594.
PR 13-SEP-1999; 99MO-US020944.
PR 15-SEP-1999; 99MO-US021090.
PR 15-SEP-1999; 99MO-US021547.

PR 05-OCT-1999; 99MO-US023089.
PR 29-NOV-1999; 99MO-US028214.
PR 30-NOV-1999; 99MO-US028313.
PR 30-NOV-1999; 99MO-US028409.
PR 01-DEC-1999; 99MO-US028301.
PR 01-DEC-1999; 99MO-US028634.
PR 02-DEC-1999; 99MO-US028551.
PR 02-DEC-1999; 99MO-US028564.
PR 16-DEC-1999; 99MO-US030095.
PR 20-DEC-1999; 99MO-US030911.
PR 22-DEC-1999; 99MO-US030929.
PR 22-DEC-1999; 99MO-US030720.
PR 30-DEC-1999; 99MO-US031243.
PR 30-DEC-1999; 99MO-US031274.
PR 05-JAN-2000; 2000MO-US000219.
PR 06-JAN-2000; 2000MO-US000277.
PR 06-JAN-2000; 2000MO-US000376.
PR 11-FEB-2000; 2000MO-US003565.
PR 18-FEB-2000; 2000MO-US004341.
PR 18-FEB-2000; 2000MO-US004342.
PR 22-FEB-2000; 2000MO-US004414.
PR 24-FEB-2000; 2000MO-US004514.
PR 24-FEB-2000; 2000MO-US004514.
PR 24-FEB-2000; 2000MO-US005004.
PR 01-MAR-2000; 2000MO-US005601.
PR 02-MAR-2000; 2000MO-US005746.
PR 02-MAR-2000; 2000MO-US005841.
PR 15-MAR-2000; 2000MO-US006884.
PR 20-MAR-2000; 2000MO-US007377.
PR 21-MAR-2000; 2000MO-US007532.
PR 30-MAR-2000; 2000MO-US008439.
PR 17-MAY-2000; 2000MO-US013705.
PR 22-MAY-2000; 2000MO-US014042.
PR 30-MAY-2000; 2000MO-US014941.
PR 02-JUN-2000; 2000MO-US015264.
PR 28-JUL-2000; 2000MO-US020710.
PR 11-AUG-2000; 2000MO-US022031.
PR 23-AUG-2000; 2000MO-US023522.
PR 24-AUG-2000; 2000MO-US023328.
PR 08-NOV-2000; 2000MO-US030952.
PR 10-NOV-2000; 2000MO-US030873.
PR 01-DEC-2000; 2000MO-US032678.
PR 20-DEC-2000; 2000MO-US0747259.
PR 20-DEC-2000; 2000MO-US034956.
PR 28-FEB-2001; 2001MO-US0796498.
PR 28-FEB-2001; 2001MO-US006520.
PR 01-MAR-2001; 2001MO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001MO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001MO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001MO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001MO-US020116.
PR 29-JUN-2001; 2001MO-US021066.
PR 09-JUL-2001; 2001MO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX

PA (GETH) GENENTECH INC.
XX Baker KP, Beresini M, DeGeorge L, Desnoyers L, Flivaroff B, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TR, Tumas D, Watanabe CK, Wood WJ, Zhang Z;
XX WPI; 2004-021079/02.
DR P-PSDB; ADB18484.
XX
PT New isolated nucleic acid encoding a PRO polypeptide, e.g. PRO1114 or
PT PRO4978, for use in molecular biology, chromosome and gene mapping, in
PT generating antisense RNA and DNA, and in gene therapy.
XX
XX Claim 2; SEQ ID NO 481; 638pp; English.
XX
CC The invention relates to isolated human PRO polypeptides (secreted and
CC transmembrane polypeptides) and the polynucleotides encoding them. The
CC invention also relates to an antibody which specifically binds to a PRO
CC polypeptide, a method for stimulating the release of tumour necrosis
CC factor-alpha (TNF-alpha) from human blood, a method for stimulating the
CC proliferation or differentiation of chondrocyte cells and a method for
CC detecting the presence of a tumour in a mammal (e.g. adrenal, lung,
CC colon, breast, prostate, rectal, kidney, cervical and liver tumours). The
CC polynucleotides are useful in molecular biology, including uses as
CC hybridisation probes, in chromosome and gene mapping, in generating
CC antisense RNA and DNA and in gene therapy. The polynucleotides may also
CC be used in preparing PRO polypeptides by recombinant techniques and in
CC generating either transgenic animals or knock-out animals which are
CC useful in the development and screening of therapeutically useful
CC reagents. The PRO polypeptides or antibodies are used in preparing a
CC medicament for treating a condition responsive to the polypeptides or
CC antibodies, such as tumours, for stimulating and inhibiting proliferation
CC of human microvascular endothelial cells, for modulating the uptake of
CC glucose or PEP by skeletal muscle cells or adipocyte cells, for
CC stimulating differentiation of adipocyte cells, for stimulating
CC proliferation of or gene expression in pericyte cells, for stimulating
CC the proliferation of inner ear utricular supporting cells or T-lymphocyte
CC cells, for inducing endothelial cell tube formation and for treating
CC various bone and/or cartilage disorders such as sports injuries and
CC arthritis. PRO polypeptides which stimulate the release of proteoglycans
CC from cartilage are useful for treating sports-related joint problems,
CC articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO
CC polypeptides are also useful for treating various mammalian haemoglobin-
CC associated disorders such as various thalassemias and conditions which
CC may benefit from enhanced local immune system cell infiltration. This
CC sequence represents a human PRO polynucleotide of the invention. Note:
CC The sequence data for this patent is also available in electronic format
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;
Query March 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.6e-262;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAAGAAATGTTGCTGCTCTTTTCTGAGACTGCATTCAAGCTGACTCTGCA 60
DB 1 GAAAGAAATGTTGCTGCTCTTTTCTGAGACTGCATTCAAGCTGACTCTGCA 60
QY 61 CCAAGTGCAGAAATGCTTTTAAAGTGAAGCTTAATCAAGCAAGCTCTGGAGATATA 120
DB 61 CCAAGTGCAGAAATGCTTTTAAAGTGAAGCTTAATCAAGCAAGCTCTGGAGATATA 120
QY 121 GCATATGCTGGAGATCCAAATGAATACCTCTTCAAGAGATGTAAGCTTCCCAAG 180
DB 121 GCATATGCTGGAGATCCAAATGAATACCTCTTCAAGAGATGTAAGCTTCCCAAG 180
QY 181 AGAAAGATCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 240
DB 181 AGAAAGATCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 240
QY 241 CAGAGGATATCATCTGTTGTGTGTTACAGACCTTCAAAAATCAACCTTCTGCT 300
DB 241 CAGAGGATATCATCTGTTGTGTGTTACAGACCTTCAAAAATCAACCTTCTGCT 300

DB 241 CAGAGGATATCATCTGTTGTGTGTTACAGACCTTCAAAAATCAACCTTCTGCT 300
QY 301 GTTGAAGTCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 360
DB 301 GTTGAAGTCAATCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 360
QY 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCACACTTGCACCAACCCATGACCA 420
DB 361 AATGACCAAACTCTGGAATTTTAAATCCCTTCACACTTGCACCAACCCATGACCA 420
QY 421 TCTGAGCCATCTGATATATATATGTTGATATATTTGATATATGATATGATATAT 480
DB 421 TCTGAGCCATCTGATATATATATGTTGATATATTTGATATATGATATATGATATAT 480
QY 481 GCACTACTGATTTTATCAAGGATCTGGCAACTAGAGAAAGCAAGCAAGCAAGCAAGCA 540
DB 481 GCACTACTGATTTTATCAAGGATCTGGCAACTAGAGAAAGCAAGCAAGCAAGCAAGCA 540
QY 541 GTGATGACGCTGAAGATTAAGTGAAACATGATCACAATGAAATGCAATCCCTCT 600
DB 541 GTGATGACGCTGAAGATTAAGTGAAACATGATCACAATGAAATGCAATCCCTCT 600
QY 601 GATCCCTCTGAGAGAGGCTGTTGCTCTCTCAAGAAATTAACATTTGTTCTGT 720
DB 601 GATCCCTCTGAGAGAGGCTGTTGCTCTCTCAAGAAATTAACATTTGTTCTGT 720
QY 721 GTGACTGCTGACATCTGAAATTAACAGAGATCATATATTTGTTCAACATCTT 780
DB 721 GTGACTGCTGACATCTGAAATTAACAGAGATCATATATTTGTTCAACATCTT 780
QY 781 CTTTGTATATATTTTGAATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 840
DB 781 CTTTGTATATATTTTGAATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 840
QY 841 ACCACGAAATCATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 900
DB 841 ACCACGAAATCATTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 900
QY 901 TAGTGTATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 960
DB 901 TAGTGTATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 960
QY 961 AGATGAGGATATGATATATATTTTCAACTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1020
DB 961 AGATGAGGATATGATATATATTTTCAACTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1020
QY 1021 GTGAGAAATACATATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1080
DB 1021 GTGAGAAATACATATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1080
QY 1081 CTTATATCACTCTGATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1140
DB 1081 CTTATATCACTCTGATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1140
QY 1141 TGGATATATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1200
DB 1141 TGGATATATATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1200
QY 1201 GTTGAATATATATTTTCAATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1260
DB 1201 GTTGAATATATATTTTCAATATGCTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1260
QY 1261 TCTACATATTTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1320
DB 1261 TCTACATATTTGTAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 1320
QY 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346
DB 1321 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 205
ID ADE88792 standard; cDNA; 1346 BP.
AC ADE88792;
DT 29-JAN-2004 (first entry)
XX
XX Human PRO polynucleotide #241.
DE
XX
XX Human: Gene; ss; PRO; secreted polypeptide; transmembrane polypeptide;
tumor necrosis factor-alpha; TNF-alpha; chondrocyte cell; tumour;
cancer; adrenal; lung; colon; breast; prostate; rectum; kidney; cervix;
liver; microvascular endothelial cell; glucose; FFA;
skeletal muscle cell; adipocyte cell; pericyte cell;
inner ear utricular supporting cell; T-lymphocyte cell;
endothelial cell tube formation; bone disorder; cartilage disorder;
sports injury; proteoglycan; articular cartilage defect; osteoarthritis;
rheumatoid arthritis; haemoglobin-associated disorder thalassemia;
immune system cell infiltration.
OS Homo sapiens.
XX
XX US2003199054-A1.
XX
XX 23-OCT-2003.
PF 12-APR-2002; 2002US-00121054.
XX
XX 31-MAR-1997; 97WO-US005230.
XX 12-JUN-1998; 98WO-US012456.
XX 14-JUL-1998; 98WO-US014552.
XX 28-AUG-1998; 98WO-US017888.
XX 10-SRP-1998; 98WO-US018824.
XX 14-SRP-1998; 98WO-US019093.
XX 14-SRP-1998; 98WO-US019177.
XX 14-SRP-1998; 98WO-US019330.
XX 16-SRP-1998; 98WO-US019330.
XX 17-SRP-1998; 98WO-US019437.
XX 07-OCT-1998; 98WO-US021141.
XX 29-OCT-1998; 98WO-US022891.
XX 29-OCT-1998; 98WO-US022922.
XX 20-NOV-1998; 98WO-US024855.
XX 01-DEC-1998; 98WO-US025106.
XX 05-JAN-1999; 99WO-US000106.
XX 08-MAR-1999; 99WO-US005028.
XX 10-MAR-1999; 99WO-US005190.
XX 10-MAR-1999; 2000WO-US006319.
XX 20-APR-1999; 99WO-US008615.
XX 14-MAY-1999; 99WO-US010733.
XX 02-JUN-1999; 99WO-US012252.
XX 01-SRP-1999; 99WO-US020111.
XX 08-SRP-1999; 99WO-US020594.
XX 13-SRP-1999; 99WO-US020944.
XX 15-SRP-1999; 99WO-US021090.
XX 15-SRP-1999; 99WO-US021547.
XX 05-OCT-1999; 99WO-US023089.
XX 29-NOV-1999; 99WO-US028214.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028409.
XX 01-DEC-1999; 99WO-US028504.
XX 01-DEC-1999; 99WO-US028631.
XX 02-DEC-1999; 99WO-US028551.
XX 02-DEC-1999; 99WO-US028564.
XX 02-DEC-1999; 99WO-US028565.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030911.
XX 22-DEC-1999; 99WO-US030999.
XX 30-DEC-1999; 99WO-US030720.
XX 30-DEC-1999; 99WO-US031243.
XX 30-DEC-1999; 99WO-US031274.

PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005746.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802796.
PR 14-MAR-2001; 2001US-00808689.
PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 18-MAY-2001; 2001US-00854280.
PR 18-MAY-2001; 2001US-00860216.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 05-JUN-2001; 2001US-00874503.
PR 14-JUN-2001; 2001US-00882636.
PR 19-JUN-2001; 2001US-00886342.
PR 20-JUN-2001; 2001WO-US019692.
PR 21-JUN-2001; 2001US-00887879.
PR 22-JUN-2001; 2001WO-US020116.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 18-JUL-2001; 2001US-00908827.
PR 06-AUG-2001; 2001US-00924419.
PR 09-AUG-2001; 2001US-00927796.
PR 16-AUG-2001; 2001US-00931836.
PR 19-DEC-2001; 2001US-00028072.
XX
XX (GENTH) GENENTECH INC.
XX
XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff B, Gao W,
XX Gerritsen MB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
XX Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;
XX WPI; 2004-041356/04.
XX P-PSDB; ADE88793.
XX
XX Novel secreted and transmembrane polypeptides, PRO useful for treating
XX bone disorders, arthritis, heart attack, injuries, tumors, and
XX stimulating release of TNF-alpha from human blood.
XX
XX Claim 2; SEQ ID NO 481; 638bp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor- α (TNF- α) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at www.uspto.gov/sequence.htm.

Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match	100.0%;	Score 1346;	DB 10;	Length 1346;
Best Local Similarity	100.0%;	Pred. No. 1.6e-262;		

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GAAGAAAGTGTGGCTGCTCTTTTCTGTGACAGCCATCAGTGAACCTGTCAA	60
Db	1	GAAGAAAGTGTGGCTGCTCTTTTCTGTGACAGCCATCAGTGAACCTGTCAA	60
Qy	61	CCAGGTGCAGAAATATCCTTTAAAGTGAATCTTAGTATCGAAACAGCTCTGGAGATAAA	120
Db	61	CCAGGTGCAGAAATATCCTTTAAAGTGAATCTTAGTATCGAAACAGCTCTGGAGATAAA	120
Qy	121	GCATATGCTCTGGGATATCCAAATGAATATCCTTTCAAAAGCGATGGATGCTTCTCCATG	180
Db	121	GCATATGCTCTGGGATATCCAAATGAATATCCTTTCAAAAGCGATGGATGCTTCTCCATG	180
Qy	181	AGAAAGTCCCAACAGAGAGCAACAGAAATTTCCATATGCTCTTACCTTGGCAATGTAAAC	240
Db	181	AGAAAGTCCCAACAGAGAGCAACAGAAATTTCCATATGCTCTTACCTTGGCAATGTAAAC	240
Qy	241	CAGAGGGTATCAATCTGTGTTTGTTGGTTACAGACCTTCACAAAATATCAGACCTTCTGTCT	300
Db	241	CAGAGGGTATCAATCTGTGTTTGTTGGTTACAGACCTTCACAAAATATCAGACCTTCTGTCT	300
Qy	301	GTTGAGGTGCATCAGCCATTAAGATGAACAAGACCGGATTCACATGTGCTCTTCTCTA	360
Db	301	GTTGAGGTGCATCAGCCATTAAGATGAACAAGACCGGATTCACATGTGCTCTTCTCTA	360
Qy	361	AATGACCAATCTGTGAATTTTAAAAATCCCTTCACACTTGCATCCATGAGACCA	420
Db	361	AATGACCAATCTGTGAATTTTAAAAATCCCTTCACACTTGCATCCATGAGACCA	420
Qy	421	TCTGAGCCATCTGGATTTATTAATTTGGTGTATTTTGTGATCATCATAGTTGGAATT	480
Db	421	TCTGAGCCATCTGGATTTATTAATTTGGTGTATTTTGTGATCATCATAGTTGGAATT	480
Qy	481	GCACACTAGATTTTATCAGGAGATCTGGCAACGTAGAGAAAGAACAAAGAACCACTGAA	540

Db	481	GCACCTACTGATTTTATCAGGGAGCTGGCAAGTATGAAAGAAACAAAGAACCATCTGAA	540
Oy	541	GTGGATGACGCTGAGATTAAGTGTGAAACATGATCACAATTGGCAATGCCATCCCTCT	600
Db	541	GTGATATACCTGTAAGTAAAGTGTGAAACATGATCACAATTGGCAATGCCATCCCTCT	600
Oy	601	GATTCCTCTGACATGAAAGGGGGGCAATTAATGATGCTTCATGACAGAGATGAGAGGC	660
Db	601	GATTCCTCTGACATGAAAGGGGGGCAATTAATGATGCTTCATGACAGAGATGAGAGGC	660
Oy	661	TCAACCCCTCTCTGAGAGGCTGTGTCTGCTCTCTCAAGAAATTAACATTTGTTCGT	720
Db	661	TCAACCCCTCTCTGAGAGGCTGTGTCTGCTCTCTCAAGAAATTAACATTTGTTCGT	720
Oy	721	GTGACTGCTGACACTCTGAAATACCAAGCGAGATCATATATTTTGTTCACATTCCT	780
Db	721	GTGACTGCTGACACTCTGAAATACCAAGCGAGATCATATATTTTGTTCACATTCCT	780
Oy	781	CTTTTGTATTAATTTTGAATNGCTTGAAGTAAAGTAAAGCAATTAATACCAACAC	840
Db	781	CTTTTGTATTAATTTTGAATNGCTTGAAGTAAAGTAAAGCAATTAATACCAACAC	840
Oy	841	ACCACTGAATTCATTAAGCTATTCACGACTCAAAATATTTCTAAATATTTTCTGACAGTA	900
Db	841	ACCACTGAATTCATTAAGCTATTCACGACTCAAAATATTTCTAAATATTTTCTGACAGTA	900
Oy	901	TAGGTATTAATATGTGTCAATGSGTATTTGTAGTTATTTAGCATTTTGAATA	960
Db	901	TAGGTATTAATATGTGTCAATGSGTATTTGTAGTTATTTAGCATTTTGAATA	960
Oy	961	AGATCAGGCAATATGATATATTTTCAACACTCAAAAGCTTAAGGAAATTAATTTTCCA	1020
Db	961	AGATCAGGCAATATGATATATTTTCAACACTCAAAAGCTTAAGGAAATTAATTTTCCA	1020
Oy	1021	GTGAGAGATACATTAATATATGSGTATGAGAAATCATTTGAAATGATCCTTTTGAAGATCA	1080
Db	1021	GTGAGAGATACATTAATATATGSGTATGAGAAATCATTTGAAATGATCCTTTTGAAGATCA	1080
Oy	1081	CTTATATCACTCTGTATATGACTTAAGTAAACAAAAGTGAAGTATTTGTAAATGGA	1140
Db	1081	CTTATATCACTCTGTATATGACTTAAGTAAACAAAAGTGAAGTATTTGTAAATGGA	1140
Oy	1141	TGGAATAAATNGAATTAATCACTTAAGSGTGAATTTTATCCTGTATACACGCAACA	1200
Db	1141	TGGAATAAATNGAATTAATCACTTAAGSGTGAATTTTATCCTGTATACACGCAACA	1200
Oy	1201	GTGATATATATTTTCTGAATATCAGCCCTTAATAGACAATCTTATTTGTTCACATTT	1260
Db	1201	GTGATATATATTTTCTGAATATCAGCCCTTAATAGACAATCTTATTTGTTCACATTT	1260
Oy	1261	TCTACAAATTTGTAAAGTCCAATCTGTGCTTAACATTAATGAATATATCATCTCTTTT	1320
Db	1261	TCTACAAATTTGTAAAGTCCAATCTGTGCTTAACATTAATGAATATATCATCTCTTTT	1320
Oy	1321	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346	
Db	1321	AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1346	

RESULT 206
ADAS6090
ID ADAS6090 standard; DNA, 1432 BP.
XX
XX
AC
XX
ADAS6090;
DT 20-NOV-2003 (first entry)
XX
XX
DE Gene encoding human secreted protein #269.
XX
XX
IM immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
CY cytostatic; cerebrotrophic; neuroprotective; nootropic;
KM cardiovascular; antiarteriosclerotic; gene therapy;

KM human secreted protein; immune disorder; inflammation;
KM respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KM inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KM multiple sclerosis; ischemic brain injury; Parkinson's disease;
KM Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KM triple helix formation; antisense gene therapy; forensic biology; ds;
KM gene.
XX
OS Homo sapiens.
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
XX PR 19-JUL-2001; 2001US-0306171P.
XX PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
PI WPI; 2003-167512/16.
DR P-PSDB; ADA56986.
XX
XX New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
PS Claim 21; SEQ ID NO 279; 1754dp; English.

CC The invention relates to 592 new human secreted polypeptides useful for
CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC conditions, respiratory disorders, cancers, CNS disorders, or
CC neurodegenerative disorders, or polypeptides comprising an amino acid
CC sequence at least 95% identical to the new sequences. The polypeptides,
CC antibodies or antibody fragments that bind to the polypeptides, nucleic
CC acids encoding the polypeptides, agonists or antagonists that binds to
CC the polypeptides, are useful in preparing diagnostic or pharmaceutical
CC compositions for diagnosing, treating or preventing an e.g. immune
CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC polynucleotides are useful for chromosome identification, chromosome
CC mapping, for controlling gene expression through triple helix formation
CC or antisense DNA or RNA, in gene therapy, for identifying individuals
CC from minute biological samples, in forensic biology, and as hybridization
CC probes. The polypeptides are useful for as molecular weight markers on
CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC gels, to raise antibodies, for testing biological activities, and for
CC treating or preventing neural disorders, immune system disorders,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal, proliferative and/or cancerous diseases. This sequence corresponds
CC to a gene encoding one of the polypeptide of the invention. Note: The
CC sequence data for this patent did form part of the printed specification,
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.5%; Score 1325.4; DB 7; Length 1432;
Best Local Similarity 99.5%; Pred. No. 2.4e-258;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GAAGAGATGTTGGCTGCTCTTTTCTGTGACATGCAATTCATGCAACTCTGTGAA 60
DB 63 GAAGAATGTTGGCTGCTCTTTTCTGTGACATGCAATTCATGCAACTCTGTGAA 122

QY 61 CCAAGTCCAGAAAAATGCTTTTAAAGTGAAGTATGAGAACAGCTCTGGAGATGAA 120
DB 123 CCAAGTCCAGAAAAATGCTTTTAAAGTGAAGTATGAGAACAGCTCTGGAGATGAA 182
QY 121 GCATATGCTGGAGATCAATGAAAGAAATACCTCTTCAAGAGATGATGCTTCTCAATG 180
DB 183 GCATATGCTGGAGATCAATGAAAGAAATACCTCTTCAAGAGATGATGCTTCTCAATG 242
QY 181 AGAAAGTTCCTCCACAGAGAGCAAGAAATTTCCATGCTTCAATGCTTCAATGCTTCA 240
DB 243 AGAAAGTTCCTCCACAGAGAGCAAGAAATTTCCATGCTTCAATGCTTCAATGCTTCA 302
QY 241 CAGAGGATATCATCTGATGTTGTTGTTACAGACCTTCAAAAATTCACACCTTCTGCT 300
DB 303 CAGAGGATATCATCTGATGTTGTTGTTACAGACCTTCAAAAATTCACACCTTCTGCT 362
QY 301 GTTAGAGTGCATATGAGCATTAAGATGAAACAGAACCGATCAACATGCTTCTTCTTA 360
DB 363 GTTAGAGTGCATATGAGCATTAAGATGAAACAGAACCGATCAACATGCTTCTTCTTA 422
QY 361 AATGACCAAACTCTGAAATTTTAAATCCCTTCCACATGACACCAATGAGACCA 420
DB 423 AATGACCAAACTCTGAAATTTTAAATCCCTTCCACATGACACCAATGAGACCA 482
QY 421 TCTGACCATCTGATTAATTAATTTGATGATATTTGATGATATTTGATGATATTTGATG 480
DB 483 TCTGACCATCTGATTAATTAATTTGATGATATTTGATGATATTTGATGATATTTGATG 542
QY 481 GCATCTATGATTTTATGAGGATCTGCAACATGAAAGAAAGAAACCAATCTGAA 540
DB 543 GCATCTATGATTTTATGAGGATCTGCAACATGAAAGAAAGAAACCAATCTGAA 602
QY 541 GTGATGATGCTGAAAGTAAAGTGAAGAAACATGATCAATGAAATGAGATCCCTCT 600
DB 603 GTGATGATGCTGAAAGTAAAGTGAAGAAACATGATCAATGAAATGAGATCCCTCT 662
QY 601 GATCCCTCTGACATGAAAGG-GGGCATATTAATGATGCTTCAATGACAGAGATGAGAG 659
DB 663 GATCCCTCTGACATGAAAGG-GGGCATATTAATGATGCTTCAATGACAGAGATGAGAG 722
QY 660 CTGACCCCTCTGTAAGGGCTGTGTCTCTCTTCTTCAAGAAATTAACATTTGTTCTG 719
DB 723 CTGACCCCTCTGTAAGGGCTGTGTCTCTCTTCTTCAAGAAATTAACATTTGTTCTG 782
QY 720 TGTGATGCTGAGATCTGTAATTAATCAAGAGCATATATTTGTTCAACATCT 779
DB 783 TGTGATGCTGAGATCTGTAATTAATCAAGAGCATATATTTGTTCAACATCT 842
QY 780 TCTTTTGAATTAATTTTGAATGCTTGAAGTGAAGAAAGCAATTAATTAACCAACAA 839
DB 843 TCTTTTGAATTAATTTTGAATGCTTGAAGTGAAGAAAGCAATTAATTAACCAACAA 902
QY 840 CACCACTGAATCAATTAAGCTATTAACAGCTCAAAATATTTCTTAATATTTTCTGACGT 899
DB 903 CACCACTGAATCAATTAAGCTATTAACAGCTCAAAATATTTCTTAATATTTTCTGACGT 962
QY 900 ATAGATTAATTAATGATGCTGATGTTGATGATGATGATGATGATGATGATGATGATG 959
DB 963 ATAGATTAATTAATGATGCTGATGTTGATGATGATGATGATGATGATGATGATGATG 1022
QY 960 AAGATCAGGATATGATATATTTTCAACCTTCAAGACCTTAAGAAATTAATTTTCC 1019
DB 1023 AAGATCAGGATATGATATATTTTCAACCTTCAAGACCTTAAGAAATTAATTTTCC 1082
QY 1020 AGTGAAGATCAATTAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATG 1079
DB 1083 AGTGAAGATCAATTAATTAATGCTGATGATGATGATGATGATGATGATGATGATGATG 1142
QY 1080 ACTTATATCACTGATATATGATGATGATGATGATGATGATGATGATGATGATGATG 1139
DB 1143 ACTTATATCACTGATATATGATGATGATGATGATGATGATGATGATGATGATGATG 1202


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Oy 780 TCTTTTGTATTAATTTTGGATGCTTGAAGTGAAGCAATCAATTATCCACCA 839
Db 843 TCTTTTGTATTAATTTTGGATGCTTGAAGTGAAGCAATCAATTATCCACCA 902
Oy 840 CACCACTGAATATGATAGCTATCAGACCTCAAAATTTCTAAATTTTTCGACGT 899
Db 903 CACCACTGAATATGATAGCTATCAGACCTCAAAATTTCTAAATTTTTCGACGT 962
Oy 900 ATAGTATTAATATGCTGATGCTGATTTTGTAGTTATTAAGCATTTTGAAGAT 959
Db 963 ATAGTATTAATATGCTGATGCTGATTTTGTAGTTATTAAGCATTTTGAAGAT 1022
Oy 960 AAGATCAGCATATGATATATTTTCACTTCAAGACCTTAAGAAAAATTTTTC 1019
Db 1023 AAGATCAGCATATGATATATTTTCACTTCAAGACCTTAAGAAAAATTTTTC 1082
Oy 1020 AGTGGAGATACATATATATGCTGATGATTAATCAATGAAATGCTTTTGAAGATC 1079
Db 1083 AGTGGAGATACATATATATGCTGATGATTAATCAATGAAATGCTTTTGAAGATC 1142
Oy 1080 ACTTATATACCTCTGTATATGACATAGTAAACAAAGTGAAGATATTTGTAATG 1139
Db 1143 ACTTATATACCTCTGTATATGACATAGTAAACAAAGTGAAGATATTTGTAATG 1202
Oy 1140 ATGATATAAATGGAATTAATCTCATATACAGGATGATTTTATCTGTATACACCAAC 1199
Db 1203 ATGATATAAATGGAATTAATCTCATATACAGGATGATTTTATCTGTATACACCAAC 1262
Oy 1200 AGTGTATATATATTTTGTGAATATGAGCCCTTAATGACATTTTATTTTGACAT 1259
Db 1263 AGTGTATATATATTTTGTGAATATGAGCCCTTAATGACATTTTATTTTGACAT 1322
Oy 1260 TTCTCAATTTGTAAGTCCATCTGCTCACTTAATTAAGTATATCATCTTTT 1319
Db 1323 TTCTCAATTTGTAAGTCCATCTGCTCACTTAATTAAGTATATCATCTTTT 1382
Oy 1320 TAAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTT 1346
Db 1383 TGAATGTGAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTT 1409

RESULT 208
ADAL1489
ID ADAL1489 standard; DNA; 1432 BP.
XX
XX ADAL1489;
AC
XX
XX 06-NOV-2003 (first entry)
DT
XX
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
XX
XX cancer; inflammation; immune disorder; neurological disorder;
XX blood clotting disorder; food additive; food preservative;
XX storage capability; fat content; nutritional component; ds; gene; human.
XX
XX Homo sapiens.
XX
XX US2003055236-A1.
XX
XX 20-MAR-2003.
XX
XX 14-MAR-2002; 2002US-00097065.
XX
XX 18-DEC-1997; 97US-0068006P.
XX 18-DEC-1997; 97US-0068007P.
XX 18-DEC-1997; 97US-0068008P.
XX 18-DEC-1997; 97US-0068053P.
XX 18-DEC-1997; 97US-0068054P.
XX 18-DEC-1997; 97US-0068057P.
XX 18-DEC-1997; 97US-0068064P.
XX 18-DEC-1997; 97US-0070923P.
XX 19-DEC-1997; 97US-0068169P.
XX 19-DEC-1997; 97US-0068365P.

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PR 19-DEC-1997; 97US-0068367P.
PR 19-DEC-1997; 97US-0068368P.
PR 19-DEC-1997; 97US-0068369P.
PR 17-DEC-1998; 98MO-US027059.
PR 17-JUN-1999; 99US-00334595.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
XX Kyaw H, Wei Y, Florence KA, Duan DR, Florence C, Greene JM, Feng P,
XX Perle AM, Yu G, Janat P, Ni J;
XX
XX WPI; 2003-567105/53.
XX
XX P-PSDB; ADAL1613.
XX
XX New secreted HKAB24 nucleic acid molecules and polypeptides, useful for
XX preventing, treating, or ameliorating a medical condition, such as
XX cancer, inflammation, immune disorders, neurological and blood clotting
XX disorders.
XX
XX PS Claim 1; SEQ ID NO 17, 118bp; English.
XX
XX The invention relates to an isolated HKAB24 nucleic acid molecule. The
XX polypeptides, nucleic acids and antibodies are useful for diagnosing a
XX pathological condition or a susceptibility to a pathological condition,
XX for preventing, treating, or ameliorating a medical condition, such as
XX cancer, inflammation and other immune disorders, neurological and blood
XX clotting disorders. The nucleic acids are also useful for chromosome
XX identification, radiation hybrid mapping or long-range restriction
XX mapping. The polypeptides and antibodies are useful for providing
XX immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
XX antagonist may also be used as a food additive or preservative to
XX increase or decrease storage capabilities, fat content or other
XX nutritional components. The present sequence represents cDNA encoding a
XX novel human secreted protein. Note: The sequence data for this patent did
XX not form part of the printed specification but was obtained in electronic
XX format directly from USPTO at
XX seqdata.uspto.gov.uk/sequence.html?docid=20030055236.
XX
XX Sequence 1432 BP; 485 A; 258 G; 252 C; 437 T; 0 U; 0 Other;
XX
XX Query Match 98.5%; Score 1325.4; DB 8; Length 1432;
XX Best Local Similarity 99.5%; Pred. No. 2.4e-258;
XX Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Oy 1 GAAAGATGTTGGCTGCTCTTTTGTGATGCTGCAATTCATGCTGAACCTGTCAA 60
Db 63 GAAAGATGTTGGCTGCTCTTTTGTGATGCTGCAATTCATGCTGAACCTGTCAA 122
Oy 61 CCAAGTGCAGAAATGCTTTTAAAGTGAAGTATGATCAGAACAGCTTGGAGATPAA 120
Db 123 CCAAGTGCAGAAATGCTTTTAAAGTGAAGTATGATCAGAACAGCTTGGAGATPAA 182
Oy 121 GCATATGCTGGATACCAATGAAATACCTTTCAAGGATGTGCTTTCTCATG 180
Db 183 GCATATGCTGGATACCAATGAAATACCTTTCAAGGATGTGCTTTCTCATG 242
Oy 181 AGAAAGTTCCTCAACAGAGACCAAGAAATTTCCATGCTTCAATGAAATGTAAC 240
Db 243 AGAAAGTTCCTCAACAGAGACCAAGAAATTTCCATGCTTCAATGAAATGTAAC 302
Oy 241 CAGAGGATCATCTTGGTTTGTGTTAGAGACCTTCAAAAATTCACACCTTCTGCT 300
Db 303 CAGAGGATCATCTTGGTTTGTGTTAGAGACCTTCAAAAATTCACACCTTCTGCT 362
Oy 301 GTTGAAGTGAATCAAGCATTAAGATGAACAAGACCGATCAACATGCTTTCTTA 360
Db 363 GTTGAAGTGAATCAAGCATTAAGATGAACAAGACCGATCAACATGCTTTCTTA 422
Oy 361 AATGACCAACTCTGGAATTTTAAATCCCTTCCACATGACACCAATGAGACCA 420
Db 423 AATGACCAACTCTGGAATTTTAAATCCCTTCCACATGACACCAATGAGACCA 482

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[illegible]

RESULT	209
	ADD37613
ID	ADD37613 standard; cDNA; 1432 BP
XX	
AC	ADD37613;
XX	
DT	15-JAN-2004 (first entry)

DB	Sequence	Human secreted protein encoding sequence #95.
XX	Human secreted protein encoding sequence #95.	
XX	human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;	
XX	Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.	
XX	Homo sapiens.	
XX	MO200290526-A2.	
XX	14-NOV-2002.	
XX	19-MAR-2002; 2002MO-US008279.	
XX	21-MAR-2001; 2001US-0277340P.	
XX	19-JUL-2001; 2001US-0306171P.	
XX	13-NOV-2001; 2001US-0331287P.	
XX	(HOMA-) HUMAN GENOME SCI INC.	
XX	Rosen CA, Ruben SM;	
XX	WPI; 2003-140218/13.	
XX	New human secreted proteins and nucleic acid molecules, useful for	
XX	preparing a diagnostic or pharmaceutical composition for diagnosing or	
XX	treating allergic or asthmatic disorders, or related immediate	
XX	hypersensitivity disorders.	
XX	Claim 7; SEQ ID NO 95; 1333pp; English.	
XX	The present invention relates to an isolated polypeptide or human	
XX	secreted protein. The polypeptides, nucleic acid molecules, antibodies or	
XX	their fragments, and agonists or antagonists that bind are useful for	
XX	preparing a diagnostic or pharmaceutical composition for diagnosing or	
XX	treating allergic or asthmatic disorders. The polypeptide is also useful	
XX	for identifying a binding partner by contacting the polypeptide with a	
XX	binding partner, and determining whether the binding partner increases or	
XX	decreases the activity of the polypeptide. The polypeptides and nucleic	
XX	acid molecules are also useful for detecting, preventing, diagnosing,	
XX	prophylactically, treating or ameliorating inflammatory disorders	
XX	neoplastic diseases, wound healing and disorders of epithelial cell	
XX	proliferation, immune disorders, cardiovascular disorders, blood-related	
XX	disorders, infectious diseases, endocrine disorders, or gastrointestinal	
XX	disorders. The nucleic acids are also useful for chromosome	
XX	identification, radiation hybrid mapping or long-range restriction	
XX	mapping, as molecular weight markers, or as hybridization or diagnostic	
XX	probes. The polypeptides and antibodies are useful for providing	
XX	immunological probes for differential identification of the tissues	
XX	immunohistochemistry assays. The present sequence represents a human	
XX	secreted protein encoding sequence.	
XX	Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;	
XX	Query Match 98.5%; Score 1325.4; DB 9; Length 1432;	
XX	Best Local Similarity 99.5%; Pred. No. 2.4e-256;	
XX	Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;	
DB	1 GAAAGAAAGTGTGAGCTCTCTTTTCTGTGACTGGCATTCATGCTGAATCTGTCTCA 60	
DB	63 GAAAGAAATGTGTGCTGCTCTCTTTTCTGTGACTGGCATTCATGCTGAATCTGTCTCA 122	
QY	61 CCAAGTGCAGAAATGCTTTTAAAGTGAAGTATGATCAGAACAGCTCTGGAGATTA 120	
DB	123 CCAAGTGCAGAAATGCTTTTAAAGTGAAGTATGATCAGAACAGCTCTGGAGATTA 182	
QY	121 GCATTTGCTGGGATCCAAAGAAAGATACCTCTTCAAAGGATGTAGCTTCTCCATG 180	
DB	183 GCATTTGCTGGGATCCAAAGAAAGATACCTCTTCAAAGGATGTAGCTTCTCCATG 242	
QY	181 AGAAAGATCCCAAGAGAGCAAGAAATTTCCATGTCTACTTGTGCAATGTAAAC 240	
DB	243 AGAAAGATCCCAAGAGAGCAAGAAATTTCCATGTCTACTTGTGCAATGTAAAC 302	

QY	241	CAGAGGGATCAATCTGGTTTGTTGGTTAACAACCTTCAAAAAATCACACCTTCGTCT	300
Db	303	CAGAGGGATCAATCTGGTTTGTTGGTTAACAACCTTCAAAAAATCACACCTTCGTCT	362
QY	301	GTTAGAGTGCAATCAGCCATTAAGATGAAACAAGAACCAGATCAACAATGCCCTTCTTCTA	360
Db	363	GTTAGAGTGCAATCAGCCATTAAGATGAAACAAGAACCAGATCAACAATGCCCTTCTTCTA	422
QY	361	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACATTCGACACCACTGGACCCA	420
Db	423	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACATTCGACACCACTGGACCCA	482
QY	421	TCCTGGCCCATCTGGAATTAATATATTTGGTGATATTTTGGCAATCAATATGTGTGAAT	480
Db	483	TCCTGGCCCATCTGGAATTAATATATTTGGTGATATTTTGGCAATCAATATGTGTGAAT	542
QY	481	GCACCTACGATTTTATCAGGGATCTGGCAAGCTGAGAGAAAGAACCAAGACATCGAA	540
Db	543	GCACCTACGATTTTATCAGGGATCTGGCAAGCTGAGAGAAAGAACCAAGACATCGAA	602
QY	541	GTGATGACGCTGAGAGATTAAGTGTGAAAAACATGATCACAATTGAAAAATGGCATCCCTCT	600
Db	603	GTGATGACGCTGAGAGATTAAGTGTGAAAAACATGATCACAATTGAAAAATGGCATCCCTCT	662
QY	601	GATCCCTCTGACATGAAAGG--GGGCATATTATGATGCTTCATGACAGAGATGAGAGG	659
Db	663	GATCCCTCTGACATGAAAGGAGGGGCAATTAATGATGCTTCATGACAGAGATGAGAGG	722
QY	660	CTCACCCCTCTCTGAAGGGCTGGTGTCTGCTCTCTCAAGAAATTAACATTTGGTCTCG	719
Db	723	CTCACCCCTCTCTGAAGGGCTGGTGTCTGCTCTCTCAAGAAATTAACATTTGGTCTCG	782
QY	720	TGTGACTGCTGAGCATCTGAAATAACAAAGACAGATCATATATTTGTTTACACATTC	779
Db	783	TGTGACTGCTGAGCATCTGAAATAACAAAGAGAGATCATATATTTGTTTACACATTC	842
QY	780	TCTTTTGTATTAATTTTGAATGTGCTTGAAAGTGAAAAAGCAATCATTAATCCACCA	839
Db	843	TCTTTTGTATTAATTTTGAATGTGCTTGAAAGTGAAAAAGCAATCATTAATCCACCA	902
QY	840	CACCACTGAATCATTAAGCTATTAACGACTCAAAATATCTTAATAATTTTCTGACAGT	899
Db	903	CACCACTGAATCATTAAGCTATTAACGACTCAAAATATCTTAATAATTTTCTGACAGT	962
QY	900	ATATGATTAATATGAGTCAATGTGATTTTGTAGTTATGCAATTTAAGCAATTTAGAAT	959
Db	963	ATATGATTAATATGAGTCAATGTGATTTTGTAGTTATGCAATTTAAGCAATTTAGAAT	1022
QY	960	AAGATCAGGCATATGTATATATATTTTCAACACTTCAAAAGCTTAAGAAAAATTAATTTCC	1019
Db	1023	AAGATCAGGCATATGTATATATATTTTCAACACTTCAAAAGCTTAAGAAAAATTAATTTCC	1082
QY	1020	AGTGAAGATCATATTAATATGTGTATGAATCATTTGAAAATGTGATCCTTTTGACATC	1079
Db	1083	AGTGAAGATCATATTAATATGTGTATGAATCATTTGAAAATGTGATCCTTTTGACATC	1142
QY	1080	ACTTATATCACTGTATATATGCTTAAGTAAACAAAAGGAGAGATTAATTTGTAATAG	1139
Db	1143	ACTTATATCACTGTATATATGCTTAAGTAAACAAAAGGAGAGATTAATTTGTAATAG	1202
QY	1140	ATGATTAATAATGAAATTAATCATATACAGGGTGAATTTTATCCTGTTATCACACCAAC	1199
Db	1203	ATGATTAATAATGAAATTAATCATATACAGGGTGAATTTTATCCTGTTATCACACCAAC	1262
QY	1200	AGTTGATTAATATTTTCTGAAATACAGCCCTTAATAGACAAATTCATTTGTTGACAT	1259
Db	1263	AGTTGATTAATATTTTCTGAAATACAGCCCTTAATAGACAAATTCATTTGTTGACAT	1322
QY	1260	TTCTACAAATTTGTAAAGGCCAATCTGGCTTAACCTAATTAAGTAAATATCATCTCTTT	1319
Db	1323	TTCTACAAATTTGTAAAGGCCAATCTGGCTTAACCTAATTAAGTAAATATCATCTCTTT	1382

0y	1320	TA	AAAAAAAAAAAAAAAAAAAAA	1346
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CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences shown
CC in AAY6224 to AAY76424 represent fragments of the secreted proteins
XX

SQ Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.4%; Score 1324.6; DB 3; Length 1447;

Best Local Similarity 99.3%; Pred. No. 3.5e-258;

Matches 1338; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

```
QY 1 GAAGAATGTTGTCCTCTTTTCTGTCGACCTTCATCTGAACTCTGCA 60
DB 71 GAAAGATGTTGTCCTCTTTTCTGTCGACCTTCATCTGAACTCTGCA 130
QY 61 CCGGTGCAAAAATGCTTTAAAGTGAAGCTTATGAGAACAGCTCTGGAGATTA 120
DB 131 CCGGTGCAAAAATGCTTTAAAGTGAAGCTTATGAGAACAGCTCTGGAGATTA 190
QY 121 GCATATGCTGGGATACCAATGAAGATGCTTCAAGGCAATGGATCTTCATG 180
DB 131 GCATATGCTGGGATACCAATGAAGATGCTTCAAGGCAATGGATCTTCATG 250
QY 181 AGAAAGTTCCTCAAGAGAGACAGAAATTTCCATGCTCTTCTTCAATGTAAC 240
DB 251 AGAAAGTTCCTCAAGAGAGACAGAAATTTCCATGCTCTTCTTCAATGTAAC 310
QY 241 CAGAGGATTCATCTGCTTTGTTGTTACAGACCTTCAAAAATACACCTTCTGCT 300
DB 311 CAGAGGATTCATCTGCTTTGTTGTTACAGACCTTCAAAAATACACCTTCTGCT 370
QY 301 GTTGAGGTGATCAGCCATGAAGATGAACAGAACCGGATCAACATGCTTCTTCTA 360
DB 371 GTTGAGGTGATCAGCCATGAAGATGAACAGAACCGGATCAACATGCTTCTTCTA 430
QY 361 AATGACCAAACTCTGAAATTTTAAAAATCCCTTCACACTTGACACCCATGACCA 420
DB 431 AATGACCAAACTCTGAAATTTTAAAAATCCCTTCACACTTGACACCCATGACCA 490
QY 421 TCTGTCCTCATCTGATTTATATATTTGCTGATATTTTTCATCATATGTTGCAAT 480
DB 491 TCTGTCCTCATCTGATTTATATATTTGCTGATATTTTTCATCATATGTTGCAAT 550
QY 481 GCACACTGATTTTATCAGGATCTGGCAAGTGAAGAAAGAAAGAACCATCTGAA 540
DB 551 GCACACTGATTTTATCAGGATCTGGCAAGTGAAGAAAGAAAGAACCATCTGAA 610
QY 541 GTGATGACGCTGAAGATTAAGTGTCAAAAATCATGATCAATGAAATGCGATCCCTCT 600
DB 611 GTGATGACGCTGAAGATTAAGTGTCAAAAATCATGATCAATGAAATGCGATCCCTCT 670
QY 601 GATCCCTCTGACATGAGGG-GGGCAATTAATGATGCTTCATGACAGAGATGAGAG 659
DB 671 GATCCCTCTGACATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
QY 660 CTCACTCCCTCTGAGAGGCTGTTGCTCTGCTTCCCTCAAGAAATTAACATTTGTTCTG 719
DB 731 CTCACTCCCTCTGAGAGGCTGTTGCTCTGCTTCCCTCAAGAAATTAACATTTGTTCTG 790
QY 720 TGTGATGCTGACATCTGAAATTAACAGAGAGATCATATATTTGTTCAACATCT 779
DB 791 TGTGATGCTGACATCTGAAATTAACAGAGAGATCATATATTTGTTCAACATCT 850
QY 780 TCTTTGTAATTAATTTGAATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 839
DB 851 TCTTTGTAATTAATTTGAATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 910
QY 840 CACCACTGAATCATATGATTCACGATCAAAATATTTCTAAATATTTTCTGACAT 899
DB 911 CACCACTGAATCATATGATTCACGATCAAAATATTTCTAAATATTTTCTGACAT 970
QY 900 ATAGTGTATTAATGCTGATGCTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 959
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DB 971 ATAGTGTATTAATGCTGATGCTGATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1030
QY 960 AAGATCAGGATATGATATATTTTCACTTCAAGAGCTTAAGAGAAATTAATTTCC 1019
DB 1031 AAGATCAGGATATGATATATTTTCACTTCAAGAGCTTAAGAGAAATTAATTTCC 1090
QY 1020 AGTGAAGATATCATATATATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1079
DB 1091 AGTGAAGATATCATATATATGCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1150
QY 1080 ACTATATATCATCTGATATATGCTATGATTAAGTGAAGTGAAGTGAAGTGAAGTGA 1139
DB 1151 ACTATATATCATCTGATATATGCTATGATTAAGTGAAGTGAAGTGAAGTGAAGTGA 1210
QY 1140 AAGATTAATAATGATATCTCATACAGGAGGAGTATTTATCTGATATCAACCAAC 1199
DB 1211 AAGATTAATAATGATATCTCATACAGGAGGAGTATTTATCTGATATCAACCAAC 1270
QY 1200 AGTTGATTAATATTTTCTGATATATCAAGCCCTTAATAGACATTTCTATTTGTTGAC 1259
DB 1271 AGTTGATTAATATTTTCTGATATATCAAGCCCTTAATAGACATTTCTATTTGTTGAC 1330
QY 1260 TTCTACAAATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1319
DB 1331 TTCTACAAATTTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1390
QY 1320 TAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1346
DB 1391 TGAATGTGAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAA 1417

RESULT 211
ADBI1650
ID ADBI1650 standard; cDNA; 1447 BP.
XX
AC ADBI1650;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human secreted polypeptide cDNA #12.
XX
KW Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
XX Alzheimer's disease; human; ss; gene.
XX
OS Synthetic.
XX
PN Homo sapiens.
XX
PD US2003100051-A1.
XX
29-MAY-2003.
XX
10-SEP-2001; 2001US-00948783.
XX
12-MAY-1998; 98US-0085093P.
XX
12-MAY-1998; 98US-0085094P.
XX
12-MAY-1998; 98US-0085105P.
XX
12-MAY-1998; 98US-0085180P.
XX
18-MAY-1998; 98US-0085206P.
XX
18-MAY-1998; 98US-0085220P.
XX
18-MAY-1998; 98US-0085221P.
XX
18-MAY-1998; 98US-0085222P.
XX
18-MAY-1998; 98US-0085233P.
XX
18-MAY-1998; 98US-0085242P.
XX
18-MAY-1998; 98US-0085252P.
XX
18-MAY-1998; 98US-0085272P.
XX
18-MAY-1998; 98US-0085282P.
XX
06-MAY-1999; 99WO-05009847.
XX
11-SEP-2000; 2000US-0231846P.
XX
28-JUN-2001; 2001US-00892877.
XX
(RUBEN/) RUBEN S M.
XX (FLOR/) FLORENCE K A.
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XX Key Location/Qualifiers
FH CDS 71..739
FT /note="a
FT /note="secreted protein"
XX
XX WO9832853-A2.
XX
XX 30-JUL-1998.
XX
XX 23-JAN-1998; 98MO-US001396.
XX
XX 24-JAN-1997; 97US-00788789.
XX
XX (GENY) GENETICS INST INC.
XX
XX Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
XX Spaulding V, Agostino MJ;
XX
XX WPI; 1998-427949/36.
XX
XX P-PSDB; AAM29670.
XX
XX New isolated polynucleotide(s) and secreted proteins - isolated from
XX human foetal kidney, adult brain, adult salivary gland, foetal brain and
XX adult testes cDNA libraries.
XX
XX Claim 16; Page 64-65; 109pp; English.
XX
XX The sequence is that of encoding a secreted protein. Such a protein can
XX have biological activities, e.g. nutritional activity, cytokine and cell
XX proliferation/differentiation activity, immune stimulating or suppressing
XX activity, haemopoiesis regulating activity, tissue growth activity,
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and chromolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX activity, and other activities
XX
XX Sequence 1401 BP; 458 A; 258 C; 251 G; 434 T; 0 U; 0 Other;
XX
XX Query Match 98.2%; Score 1321.8; DB 2; Length 1401;
XX Best Local Similarity 99.8%; Pred. No. 1.3e-257;
XX Matches 1334; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
XX 1 GAAAGAAATGTTGTGCTCTCTTTTCTGTGACCTGCATTCATGCTGACCTGTCAA 60
XX GAAAGAAATGTTGTGCTCTCTTTTCTGTGACCTGCATTCATGCTGACCTGTCAA 124
XX 61 CCAAGTGCAGAAATGCTTTTAAAGTGAAGCTTATGATCAAGACCTGTGAGATTA 120
XX 125 CCAAGTGCAGAAATGCTTTTAAAGTGAAGCTTATGATCAAGACCTGTGAGATTA 184
XX 121 GCATATGCTGAGATACCAATGAAGATACCTCTTCAAGAGATGATCTTCTTCAG 180
XX 185 GCATATGCTGAGATACCAATGAAGATACCTCTTCAAGAGATGATCTTCTTCAG 244
XX 181 AGAAAGATCCCAAGAGAGCAAGAAATTTCCATGCTCTTCTTCAATGATTAAC 240
XX 245 AGAAAGATCCCAAGAGAGCAAGAAATTTCCATGCTCTTCTTCAATGATTAAC 304
XX 241 CAGAGGATATCTTGTGTTTGTGTACAGACCTTCAAAAATATCACACCTTCTGT 300
XX 305 CAGAGGATATCTTGTGTTTGTGTACAGACCTTCAAAAATATCACACCTTCTGT 364
XX 301 GTTGAAGTGCATCAGCCATTAAGATGAACAGAACCGATCAACATGCTTCTTTCTA 360
XX 365 GTTGAAGTGCATCAGCCATTAAGATGAACAGAACCGATCAACATGCTTCTTTCTA 424
XX 361 AATGACCAAACTCTGAATTTTAAATCCCTTCCACTTGCACACCACTGACCA 420
XX 425 AATGACCAAACTCTGAATTTTAAATCCCTTCCACTTGCACACCACTGACCA 484
XX 421 TCTGTGCCCATGTGATATATATTTGTGTGATATTTTGTGATCATCATTTGCAATT 480

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DB 485 TCTGTGCCCATGTGATATATATTTGTGTGATATTTTGTGATCATCATTTGCAATT 544
QY 481 GCACTACTGATTTTATCAAGAGATCTGGCAACGTAGAGAGAACAGAACCATCTGA 540
DB 545 GCACTACTGATTTTATCAAGAGATCTGGCAACGTAGAGAGAACAGAACCATCTGA 604
QY 541 GTGATGACGCTGAAGATTAAGTGTGAAAACATGATCACAATTTGCAATCCCTCT 600
DB 605 GTGATGACGCTGAAGATTAAGTGTGAAAACATGATCACAATTTGCAATCCCTCT 664
QY 601 GATCCCTGAGATGAAGGG-GGGCAATTAATGATGCTTCATGACAGAGATGAGAG 659
DB 665 GATCCCTGAGATGAAGGGCAATTAATGATGCTTCATGACAGAGATGAGAG 724
QY 660 CTCACCCCTCTGGAAGGGCTGTGTGCTTCTCTCAAGAAATTAACATTTGTTCTG 719
DB 725 CTCACCCCTCTGGAAGGGCTGTGTGCTTCTCTCAAGAAATTAACATTTGTTCTG 784
QY 720 TGTGACTGCTGACATCTGAAATTAACAGAGATCATATATTTTGTTCACCATCT 779
DB 785 TGTGACTGCTGACATCTGAAATTAACAGAGATCATATATTTTGTTCACCATCT 844
QY 780 TCTTTTGTATTAATTTTGAATGCTGAAAGTGAAGAAAGCAATCAATTATCCACCA 839
DB 845 TCTTTTGTATTAATTTTGAATGCTGAAAGTGAAGAAAGCAATCAATTATCCACCA 904
QY 840 CACCACTGAATCATTAAGCTATTCACAGCTCAAAATATTTCTAAATTTTCTGACGT 899
DB 905 CACCACTGAATCATTAAGCTATTCACAGCTCAAAATATTTCTAAATTTTCTGACGT 964
QY 900 ATAGTATTAATGCTGATGCTGATGATTTGTGATTTGATTTAAGCATTTTGAAGAT 959
DB 965 ATAGTATTAATGCTGATGCTGATGATTTGTGATTTGATTTAAGCATTTTGAAGAT 1024
QY 960 AAGATCAGGATATGATATATTTTCAACCTCAAGACCTAAGAGAAATTAATTTTCC 1019
DB 1025 AAGATCAGGATATGATATATTTTCAACCTCAAGACCTAAGAGAAATTAATTTTCC 1084
QY 1020 AGTGAAGATATATTAATGATGATGAAGATCATTTGAAGATCTTTTGTGACATC 1079
DB 1085 AGTGAAGATATATTAATGATGATGAAGATCATTTGAAGATCTTTTGTGACATC 1144
QY 1080 ACTTATATCATCTGTATATGACTAAGTAAACAAAGTGAAGATTAATTTGTAATG 1139
DB 1145 ACTTATATCATCTGTATATGACTAAGTAAACAAAGTGAAGATTAATTTGTAATG 1204
QY 1140 ATGATTAATTAATGAAATTAATCAATTAACAGGGTGAATTTTCTGTATCAACCAAC 1199
DB 1205 ATGATTAATTAATGAAATTAATCAATTAACAGGGTGAATTTTCTGTATCAACCAAC 1264
QY 1200 AGTGAATTAATTTTCTGAATATCAAGCCCTAATAGACAAATTTGTTGACAT 1259
DB 1265 AGTGAATTAATTTTCTGAATATCAAGCCCTAATAGACAAATTTGTTGACAT 1324
QY 1260 TTCTTACATTTTGAAGTCAATCTGTCTAATTTAATTAATTAATCAATCTCTTT 1319
DB 1325 TTCTTACATTTTGAAGTCAATCTGTCTAATTTAATTAATTAATCAATCTCTTT 1384
QY 1320 TAAAAAATTAATTAATTTTGAAGTCAATCTGTCTAATTTAATTAATTAATCAATCTCTTT 1336
DB 1385 AAAAAAATTAATTAATTTTGAAGTCAATCTGTCTAATTTAATTAATTAATCAATCTCTTT 1401

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RESULT 213
AA94470
ID AA94470 standard; cDNA; 1347 BP.
XX AA94470;
AC
XX 04-JUN-2001 (first entry)
DT
XX Human hydrophobic domain containing protein clone HP10720 cDNA #84.
XX

KW Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW antineoplastic; vulnery; anticulcer; osteoplastic; anti-inflammatory;
KW cytotoxic; gene therapy; autoimmune disorder; multiple sclerosis;
KW HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW behavioural characteristic; immune response; ss.
OS Homo sapiens.
XX MO200112660-A2.
XX 22-FEB-2001.
XX 10-AUG-2000; 2000MO-JP005356.
XX 17-AUG-1999; 99JF-00230344.
XX 07-SEP-1999; 99JF-00252551.
XX 01-OCT-1999; 99JF-00281132.
XX 22-OCT-1999; 99JF-00301624.
XX 04-NOV-1999; 99JF-00313877.
PA (SAGA) SAGAMI CHEM RES. CENT.
PA (PROT-) PROTEGENE INC.
PI Kato S, Kilmura T;
XX MPI: 2001-160059/16.
XX P-PSDB; AAB88580.
XX Human proteins with hydrophobic domains and the DNAs which encode them
XX are useful for treating autoimmune disorders, burns and tumors and for
XX screening novel pharmaceuticals.
PS Claim 4; Page 384-386; 518bp; English.
XX AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
XX AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
XX anti-HIV, neuroprotective, antineoplastic, vulnery, anticulcer,
XX osteoplastic, anti-inflammatory and cytostatic activities, and can be used
XX in gene therapy. (I) can be used as pharmaceuticals and as antigens to
XX prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
XX for genetic diagnosis and gene sources for gene therapy or for producing
XX (I) in large quantities. Cells containing (II) are used for the detection
XX of ligands or receptors corresponding to membrane or secretory proteins
XX and to screen small molecule novel pharmaceuticals. Antibodies directed
XX to (I) can be used for the detection, quantification and purification of
XX (I). Activities of (I) may include cytokine and cell
XX proliferation/differentiation function, immune stimulating or suppressing
XX activity, haematopoiesis regulating activity, tissue growth activity,
XX actin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, receptor/ligand activity and anti-inflammatory
XX activity. (I) and (II) can be used to treat autoimmune disorders e.g.
XX multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
XX inflammatory bowel disease and tumours. (I) and (II) can also be used for
XX wound healing, as nutritional sources or supplements e.g. as amino acid,
XX carbon or nitrogen source, to effect metabolism, catecholism, anabolism,
XX processing and utilisation of dietary fat, protein, carbohydrate,
XX vitamins and minerals, to effect behavioural characteristics, to affect
XX appetite, and can act as antigens in vaccines to raise an immune response
XX to the protein or another material cross-reactive with the protein
SQ Sequence 1347 BP; 434 A; 252 C; 243 G; 418 T; 0 U; 0 Other;
Query Match 97.3%; Score 1309.4; DB 4; Length 1347;
Best Local Similarity 99.8%; Pred. No. 4e-255;
Matches 131; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 GAAGAATGTTGGCTGCTCTTTTCTGATGACCTGATTCATGCTGAACCTGTCGA 60
DB 20 GAAGAATGTTGGCTGCTCTTTTCTGATGACCTGATTCATGCTGAACCTGTCGA 79
QY 61 CCAAGTGCAGAAAATGCTTTAAAGTGAAGATTAGTACGAAACAGCTCTGGAGATGAA 120

DB 80 CCAAGTGCAGAAAATGCTTTAAAGTGAAGATTAGTACGAAACAGCTCTGGAGATGAA 139
QY 121 GCATATGCTGGAATACCAATGAAGAAATACCTCTTCAAGGAGATGATGCTTCTCATG 180
DB 140 GCATATGCTGGAATACCAATGAAGAAATACCTCTTCAAGGAGATGATGCTTCTCATG 199
QY 181 AGAAAAGTCCCAACAGAGAACCAAGAAATTTCCATGCTTCACTTTGCAATGTAAC 240
DB 200 AGAAAAGTCCCAACAGAGAACCAAGAAATTTCCATGCTTCACTTTGCAATGTAAC 259
QY 241 CAGAGGATATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 300
DB 260 CAGAGGATATCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 319
QY 301 GTTGAAGTGCAGAACCAATGAAGAAATGGAACCAAGGATCAATGAGCTTCTTCTCA 360
DB 320 GTTGAAGTGCAGAACCAATGAAGAAATGGAACCAAGGATCAATGAGCTTCTTCTCA 379
QY 361 AATGACCAAACTCTGGAATTTTAAATATCCCTTCCACACTTGCACCAACCAATGACCA 420
DB 380 AATGACCAAACTCTGGAATTTTAAATATCCCTTCCACACTTGCACCAACCAATGACCA 439
QY 421 TCTGTGCTCCATCTGATTTATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
DB 440 TCTGTGCTCCATCTGATTTATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 499
QY 481 GCATATGCTGGAATACCAATGAAGAAATACCTCTTCAAGGAGATGATGCTTCTCATG 540
DB 500 GCATATGCTGGAATACCAATGAAGAAATACCTCTTCAAGGAGATGATGCTTCTCATG 559
QY 541 GTGATGACGCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
DB 560 GTGATGACGCTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 619
QY 601 GATCCCTCTGACATGAAGG-GGGCAATTTATGATGCTTCTCAAGGAGATGATGATGAT 659
DB 620 GATCCCTCTGACATGAAGG-GGGCAATTTATGATGCTTCTCAAGGAGATGATGATGAT 679
QY 660 CTCACCCCTCTGAAAGGGGCTGTTCTGCTTCTCAAGAAATTTAACTTTGTTCTG 719
DB 680 CTCACCCCTCTGAAAGGGGCTGTTCTGCTTCTCAAGAAATTTAACTTTGTTCTG 739
QY 720 TGTGACTGCTGAGCATCTGAATATCAAGAGCATCATATATTTGTTTCACTTCT 779
DB 740 TGTGACTGCTGAGCATCTGAATATCAAGAGCATCATATATTTGTTTCACTTCT 799
QY 780 TCTTTGTTATTAATTTGATGATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 839
DB 800 TCTTTGTTATTAATTTGATGATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 859
QY 840 CACCACTGAATCATAGATATTCACAGCTCAAAATTTCTTAAATTTTCTTCAAGT 899
DB 860 CACCACTGAATCATAGATATTCACAGCTCAAAATTTCTTAAATTTTCTTCAAGT 919
QY 900 ATAGTATTAATTTGATGATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 959
DB 920 ATAGTATTAATTTGATGATGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 979
QY 960 AAGATCGGATATGATATTTTCACTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1019
DB 980 AAGATCGGATATGATATTTTCACTTCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1039
QY 1020 AGTGAAGATATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 1040 AGTGAAGATATATATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1099
QY 1080 ACTTATATCACTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
DB 1100 ACTTATATCACTGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1159
QY 1140 ATGATATTAATATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
DB 1160 ATGATATTAATATGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1219

QY 1200 AGTGAATATATATATTTCTGAATATACAGCCCTATATAGACAATCTATTTGTGACCAT 1259
DB 1220 AGTGAATATATATATTTCTGAATATACAGCCCTATATAGACAATCTATTTGTGACCAT 1279
QY 1260 TTCTACATTTGTAAAGTCCATCTGTCTAATTAATTAATATATATCTCTTTT 1319
DB 1280 TTCTACATTTGTAAAGTCCATCTGTCTAATTAATTAATATATATATCTCTTTT 1339
QY 1320 TAA 1322
DB 1340 TGA 1342

RESULT 214
ABZ78127
ID ABZ78127 standard; cDNA; 1345 BP.
XX ABZ78127;
AC
XX 19-MAY-2003 (first entry)
DT
XX
DE Human cancer-related coding sequence, 156P1D4.
XX
XX Human; cytosolic; vaccine; cancer; immune response; gene; ss.
OS Homo sapiens.
XX
XX W0200283921-A2.
XX
XX 24-OCT-2002.
PD
XX 10-APR-2002; 2002MO-US011654.
PF
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakubovics A, Challita-Eld PM, Paris W, Ge W, Hubert RS,
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI: 2003-075555/07.
DR P-PSDB: ABR01796.
XX
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

Claim 26; Fig 2G; 1021p; English.

The present invention relates to novel human cancer-related genes and
proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
proteins are useful for eliciting a humoral or cellular immune response.
The genes are useful as probes and primers for the amplification and/or
detection of genes, mRNAs or their fragments, as reagents for the
diagnosis and/or prognosis of cancer, as coding sequences capable of
inhibiting the expression of the protein, as tools for modulating or
controlling the expression of genes and/or translation of transcripts, and
as therapeutic agents. The proteins and peptides are useful as
therapeutic, prognostic and diagnostic reagents for cancer. 74P1B3 maps
to chromosome 8p21.3-p22, 83P4B8 maps to chromosome 15q25.1, 109P1D4 maps
to chromosome Xq21.3, 151P1C7A maps to chromosome 10q11.2, 151P4E11 maps
to chromosome 11q13.3-q13.5, 154P2A8 maps to chromosome 3q24, 156P1D4
maps to chromosome Xp22.3, 156P5C12 maps to chromosome 2p13.1-p12,
159P2B5 maps to chromosome 7p15.1, 161P2B7A maps to chromosome 3q25-q26,
179P3C7 maps to chromosome 12q12-q13, 144P3C10B maps to chromosome
19p13.1, 184P3G10 maps to chromosome 2p12, 185P2C9 maps to chromosome
18p11.22, 185P3C3 maps to chromosome 17q21, 185P1H9 maps to chromosome
7q21.3-q22.1, 187P3F2 maps to chromosome 3p14.2 and 192P2G7 maps to
chromosome 22q13.2-q13.31

XX
SQ Sequence 1345 BP; 435 A; 251 C; 241 G; 418 T; 0 U; 0 Other;
Query Match 97.2%; Score 1307.8; DB 7; Length 1345;
Best Local Similarity 99.8%; Pred. No. 8.5e-255;
Matches 1320; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

1 GAAAGAAATGTTGCTGCTCTCTTTTCTGTGATCTGCATTCATGCTGATCA 60
DB GAAAGAAATGTTGCTGCTCTCTTTTCTGTGATCTGCATTCATGCTGATCA 77
QY 61 CCAAGTGCAGAAAATGCTTTTAAAGTGAAGCTTACTATCAGAACAGCTCTGGAGATTA 120
DB 78 CCAAGTGCAGAAAATGCTTTTAAAGTGAAGCTTACTATCAGAACAGCTCTGGAGATTA 137
QY 121 GCATATGCTGCGAATACCAATGAATATCCTCTCAAGAGCAATGCTTCTCCAG 180
DB 138 GCATATGCTGCGAATACCAATGAATATCCTCTCAAGAGCAATGCTTCTCCAG 197
QY 181 AGAAAAGTTCCCAACAGAGAGCAACAGAAATTTCCATGCTCTACTTGCATGTAC 240
DB 198 AGAAAAGTTCCCAACAGAGAGCAACAGAAATTTCCATGCTCTACTTGCATGTAC 257
QY 241 CAGAGGGTATCATTTCTGTTGTGTGTTACAGACCTTCAGAAAATCAGACCTTCTGCT 300
DB 258 CAGAGGGTATCATTTCTGTTGTGTGTTACAGACCTTCAGAAAATCAGACCTTCTGCT 317
QY 301 GTTGAAGTGCATTCAGCCATTAAGATGAATGAACAGAACCCGATCAAGTCCCTTTCTA 360
DB 318 GTTGAAGTGCATTCAGCCATTAAGATGAATGAACAGAACCCGATCAAGTCCCTTTCTA 377
QY 361 AATGACCAAACTCTGAAAATTTTAAATAATCCCTTCACACTTGACCAACCCATGACCA 420
DB 378 AATGACCAAACTCTGAAAATTTTAAATAATCCCTTCACACTTGACCAACCCATGACCA 437
QY 421 TCTGTGCCATCTGCAATTAATTAATTTGTGTGATATTTTGTGATCATCTAGTTGCAATT 480
DB 438 TCTGTGCCATCTGCAATTAATTAATTTGTGTGATATTTTGTGATCATCTAGTTGCAATT 497
QY 481 GCATCTAGTATTTTATCAAGGATCTGCGAACCTTAAGAGAAAGAAAGAACATCTGAA 540
DB 498 GCATCTAGTATTTTATCAAGGATCTGCGAACCTTAAGAGAAAGAAAGAACATCTGAA 557
QY 541 GTGATGACGCTGAAGATTAAGTGTGAATAATCATGATCATATGAAATGCAATCCCTCT 600
DB 558 GTGATGACGCTGAAGATTAAGTGTGAATAATCATGATCATATGAAATGCAATCCCTCT 617
QY 601 GATCCCTGACATGAAGGAGGAGGATTAATGATGATGATGATGATGATGATGATGATG 659
DB 618 GATCCCTGACATGAAGGAGGAGGATTAATGATGATGATGATGATGATGATGATGATG 677
QY 660 CTCACCCCTCTGAAAGGGCTGTTGTTCTGCTCTCAAGAAATTAACATTTGTTCTG 719
DB 678 CTCACCCCTCTGAAAGGGCTGTTGTTCTGCTCTCAAGAAATTAACATTTGTTCTG 737
QY 720 TGTGATGCTGAGCATCTGAAATTAAGTGTGAATAATCATGATCATATGAAATGCAATCC 779
DB 738 TGTGATGCTGAGCATCTGAAATTAAGTGTGAATAATCATGATCATATGAAATGCAATCC 797
QY 740 TCTTTTGTAAATTTTGAATGCTGAAAGTGAATAATCATGATCATATGAAATGCAATCC 839
DB 758 TCTTTTGTAAATTTTGAATGCTGAAAGTGAATAATCATGATCATATGAAATGCAATCC 857
QY 840 CACCACTGAATCATTAAGCTATTCAGCTCAAAATATTTTAAATTTTCTGACAGT 899
DB 858 CACCACTGAATCATTAAGCTATTCAGCTCAAAATATTTTAAATTTTCTGACAGT 917
QY 900 ATAGTATTAATTAATGCTATGCTATGCTATTTGATGATGATTAAGCAATTTTGAAT 959
DB 918 ATAGTATTAATTAATGCTATGCTATGCTATTTGATGATGATTAAGCAATTTTGAAT 977
QY 960 AAGATGAGCATATGATATATTTTCAACATTCAGAAAGCTTAAGAAATTAATTTTCC 1019

Db	978	AAGATCAGGCAATATGTATATATATTTTTCACACTTCAGGAGACCTTAGAGAAAATAATTTTCC	1037
Qy	1020	AGTGGAGATACATATTAATANGTGTAGAAAATCATTTGAAATGATCCTTTTTCAGCATC	1079
Db	1038	AGTGGAGATACATATTAATANGTGTAGAAAATCATTTGAAATGATCCTTTTTCAGCATC	1097
Qy	1080	ACTTATATCATCTGTATATATGACTTAAGTAAACAAAAGTGAAGTATTTATTTGTAATGG	1139
Db	1098	ACTTATATCATCTGTATATATGACTTAAGTAAACAAAAGTGAAGTATTTATTTGTAATGG	1157
Qy	1140	ATGATATAAAATGGAATTACATCATATACAGGGTGAATTTTATCCTGTATACACCAAC	1199
Db	1158	ATGATATAAAATGGAATTACATCATATACAGGGTGAATTTTATCCTGTATACACCAAC	1217
Qy	1200	AGTTGATTATATATATTTCTGCAATATACAGCCCTTAATAGACAAATCTATTTGTTGACAT	1259
Db	1218	AGTTGATTATATATATTTCTGCAATATACAGCCCTTAATAGACAAATCTATTTGTTGACAT	1277
Qy	1260	TTCTTCGAATTTGTAAAGTCCATCTGTGCTTACTTAATTAAGTAAATATATGATCTCTTTT	1319
Db	1278	TTCTTCGAATTTGTAAAGTCCATCTGTGCTTACTTAATTAAGTAAATATATGATCTCTTTT	1337
Qy	1320	TAA 1322	
Db	1338	TGA 1340	
RESULT 215			
AAH98224/C			
ID	AAH98224	standard; cDNA; 1365 BP.	
AC	AAH98224;		
XX			
DT	12-OCT-2001	(first entry)	
XX			
DE	Human EST-derived coding sequence SEQ ID NO: 81.		
XX			
KW	Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;		
KW	tomato; monkey; dog; sea urchin; expressed sequence tag; EST;		
KW	diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;		
KW	gene therapy; nutrition; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200154477-A2.		
XX			
PD	02-AUG-2001.		
XX			
PE	25-JAN-2001; 2001WO-US002687.		
XX			
PR	25-JAN-2000; 2000US-00491404.		
PR	17-JUL-2000; 2000US-00617746.		
PR	03-AUG-2000; 2000US-00631451.		
PR	15-SEP-2000; 2000US-00663870.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aeundi V,		
PI	Cao Y, Dermanac RA, Zhang J, Werhman T,		
XX			
DR	WPI: 2001-476164/51.		
DR	P-PSDB; AAM23565.		
XX			
PT	Isolated polypeptide for treatment of diseases, diagnostics, raising		
PT	antibodies and research use.		
XX			
PS	Claim 1; Page 234; 1275pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of novel		
CC	proteins from a variety of organisms, including human, dog, cat, horse,		
CC	cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea		
CC	urchin and tomato. These were derived from expressed sequence tags (ESTs)		
CC	from the organism of interest. They can be used in diagnostics,		

CC	forensic	gene mapping	identification of mutations	to assess
CC	biodiversity	and for nutritional	purposes	The present sequence is a cDNA
CC	of the invention			
XX				
Sequence	1365 BP;	416 A;	244 C;	257 G; 448 T; 0 U; 0 Other;
Query Match	97.18;	Score 1307.4;	DB 4;	Length 1365;
Best Local Similarity	99.48;	Pred. No. 1e-254;		
Matches 1333;	Conservative	0;	Mismatches 6;	Indels 2;
			Gaps	2;
OY	1	GAAAGAAATGTTGSGCTCTCTTTTTCGTGTGACTGCCATTCATGCTGAACCTGTGTCAA	60	
DB	1341	GAAAGAAATGTTGSGCTCTCTTTTTCGTGTGACTGCCATTCATGCTGAACCTGTGTCAA	1282	
OY	61	CCAGGTGCAGAAAATGCTTTTAAAGTAGACTTATGATTCAGAACAGCTCTGGAGATAA	120	
DB	1281	CCAGGTGCAGAAAATGCTTTTAAAGTAGACTTATGATTCAGAACAGCTCTGGAGATAA	1222	
OY	121	GCATATGCTGGGTATCCATGAAAGATPACTCTTCAAGAGATGTAGCTTCCATG	180	
DB	1221	GCATATGCTGGGTATCCATGAAAGATPACTCTTCAAGAGATGTAGCTTCCATG	1162	
OY	181	AGAAAAGTTCCTCCACAGAGAACACAGAAATTTCCATGTCTTACTTGTGCAATGTAAAC	240	
DB	1161	AGAAAAGTTCCTCCACAGAGAACACAGAAATTTCCATGTCTTACTTGTGCAATGTAAAC	1102	
OY	241	CAGAGGGATCAATCTGGTGTGTGTGTTACAGACCTTCGAAAAATTCACACCTTCTGCT	300	
DB	1101	CAGAGGGATCAATCTGGTGTGTGTGTTACAGACCTTCGAAAAATTCACACCTTCTGCT	1042	
OY	301	GTTGAGGTGCAATGAGCCATPAAGATGAACAAGAACGGATTCACATGCTTCTCTA	360	
DB	1041	GTTGAGGTGCAATGAGCCATPAAGATGAACAAGAACGGATTCACATGCTTCTCTA	982	
OY	361	AATGACCAAACTCTGGAATTTTAAATATCCCTTCCACACTTGTGACCAACCCATGACCCA	420	
DB	981	AATGACCAAACTCTGGAATTTTAAATATCCCTTCCACACTTGTGACCAACCCATGACCCA	922	
OY	421	TCTGTGCCCATCTGGAATTTATATTTGTGTGATTTTGTGATCATCATATGTTGCAATT	480	
DB	921	TCTGTGCCCATCTGGAATTTATATTTGTGTGATTTTGTGATCATCATATGTTGCAATT	862	
OY	481	GCATCTACGATTTTATCAAGGATCTGTGCAACGTGAAGAAAGACAAAGAACCATCTGAA	540	
DB	861	GCATCTACGATTTTATCAAGGATCTGTGCAACGTGAAGAAAGACAAAGAACCATCTGAA	802	
OY	541	GTGATATGACGCTGAAG-ATAAGTGTGAAACAATGATCACAATTGAAAATGGCATCTCCCTC	599	
DB	801	GTGATATGACGCTGAAGATATGATGTGAAACAATGATCACAATTGAAAATGGCATCTCCCTC	742	
OY	600	TGATCCCTCTGACATGAAAGG-GGGCAATATTAATGATGCTTCAATGACAGAGATGAGAG	658	
DB	741	TGATCCCTCTGACATGAAAGGAGGCAATATTAATGATGCTTCAATGACAGAGATGAGAG	682	
OY	659	GCTCAACCCCTCTGGAAGGGCTGTGTGTCTCTCCCAAGAAATTTAAACATTTGTTCT	718	
DB	681	GCTCAACCCCTCTGGAAGGGCTGTGTGTCTCTCCCAAGAAATTTAAACATTTGTTCT	622	
OY	719	GTGTGACGTGACGATCTCTGAATATCAAGAGAGATTCATATATTTTGTGTCAACATTC	778	
DB	621	GTGTGACGTGACGATCTCTGAATATCAAGAGAGATTCATATATTTTGTGTCAACATTC	562	
OY	779	TTCTTTTGTATATAAATTTGATGTGCTTGAAGGTGAAGAAAGCAATTCATCCACCA	838	
DB	561	TTCTTTTGTATATAAATTTGATGTGCTTGAAGGTGAAGAAAGCAATTCATTCACCA	502	
OY	839	ACACCACTGAATCATTAAGCTATTCACGACTCAAAATATTTCTAAATATTTTCTGACAG	898	
DB	501	ACACCACTGAATCATTAAGCTATTCACGACTCAAAATATTTCTAAATATTTTCTGACAG	442	
OY	899	TATGTGTATTAATATGTCATGTGATTTGTAGTTATGATTTAAGCAATTTTAAATA	958	
DB	441	TATGTGTATTAATATGTCATGTGATTTGTAGTTATGATTTAAGCAATTTTAAATA	382	

QY 959 TAAGATCAGCATATGATATATTTTCAACCTTCAAGACCTAAGAAAAATTAATTTTC 1018
DB 381 TAAATCAGCATATGATATATTTTCAACCTTCAAGACCTAAGAAAAATTAATTTTC 322
QY 1019 CAGTGAGAAATACATATATATATGATGAGAAATCAATGAAAAATGATCCTTTTGACAT 1078
DB 321 CAGTGAGAAATACATATATATATGATGAGAAATCAATGAAAAATGATCCTTTTGACAT 262
QY 1079 CACTATATCATCTCTGTATATGACCTAAGAAACAAAGAGAGAAATTAATTTGTAATG 1138
DB 261 CACTATATCATCTCTGTATATGACCTAAGAAACAAAGAGAGAAATTAATTTGTAATG 202
QY 1139 GATGATATATATGATATTAATTAATCAAGAGGAGAAATTTATCTGTATCAACCA 1198
DB 201 GATGATATATATGATATTAATTAATCAAGAGGAGAAATTTATCTGTATCAACCA 142
QY 1199 CAGTTGATATATATTTTCTGAAATATGAGCCCTTAATAGAACAAATTTATTTGACCA 1258
DB 141 CAGTTGATATATATTTTCTGAAATATGAGCCCTTAATAGAACAAATTTATTTGACCA 82
QY 1359 TTTCTACAAATTTGTAAGATCCTGCTGCTAATTAATTAATTAATCAATCTCTT 1318
DB 81 TTTCTACAAATTTGTAAGATCCTGCTGCTAATTAATTAATTAATCAATCTCTT 22
QY 1319 TTTAAAAAATTTAAAAAATTTAAAA 1339
DB 21 TTGATTTGAAAAAATTTAAAA 1

RESULT 216
AAK97957 standard; DNA; 1356 BP.
ID AAK97957 standard; DNA; 1356 BP.
AC AAK97957;
XX 17-SEP-1999 (first entry)
XX Human secreted protein gene 42.
DE Human secreted protein gene 42.
XX Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; ss.
XX Homo sapiens.
OS
XX MO9931117-A1.
XX 24-JUN-1999.
XX 17-DEC-1998; 98WO-US027059.
XX 18-DEC-1997; 97US-0068006P.
XX 18-DEC-1997; 97US-0068007P.
XX 18-DEC-1997; 97US-0068008P.
XX 18-DEC-1997; 97US-0068053P.
XX 18-DEC-1997; 97US-0068054P.
XX 18-DEC-1997; 97US-0068057P.
XX 18-DEC-1997; 97US-0068064P.
XX 18-DEC-1997; 97US-0070923P.
XX 18-DEC-1997; 97US-0068123P.
XX 18-DEC-1997; 97US-0068165P.
XX 18-DEC-1997; 97US-0068365P.
XX 18-DEC-1997; 97US-0068367P.
XX 18-DEC-1997; 97US-0068368P.
XX 18-DEC-1997; 97US-0068369P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Moore PA, Ruben SM, Carter KC, Shi Y, Roegen CA, Soppet DR;
PI Kyaw H, Wei Y, Florence K, Duan RD, Florence C, Greene JM, Feng P;

PI Ferrie AM, Yu G, Janat F, Ni U;
XX WPI: 1999-418749/35.
DR P-PSDB; AAK36265.
XX
PT New isolated human genes encoding secreted polypeptides.
PS Claim 1: Page 296-297; 537pp; English.
XX
CC AAK97916 to AAK98029 represent 110 isolated human secreted protein genes.
CC AAK36224 to AAK36727 represent the secreted proteins encoded by the 110
CC human genes. The genes and their corresponding secreted polypeptides are
CC useful for preventing, treating or ameliorating medical conditions, e.g.,
CC by protein or gene therapy. Also pathological conditions can be diagnosed
CC by determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new genes. Specific uses are
CC described for each of the 110 genes, based on which tissues they are most
CC highly expressed in, and include developing products for the diagnosis or
CC treatment of cancer, tumours, developmental abnormalities and foetal
CC deficiencies, blood disorders, diseases of the immune system, autoimmune
CC diseases, inflammation, allergies, Alzheimer's and cognitive disorders,
CC schizophrenia, arthritis, asthma, psoriasis, sepsis, skin disorders,
CC atherosclerosis, diabetes, cardiovascular disorders, kidney disorders,
CC digestive/endocrine disorders, infections and AIDS. The polypeptides are
CC also useful for identifying their binding partners. The sequences given
CC in AAK97907 to AAK97915 and AAK36223 are used in the exemplification of
CC the present invention
XX
SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;
Query Match 97.0%; Score 1305; DB 2; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
QY 1 GAAAGATTTTGTGGCTCTCTTTTCTGAGACCTGCAATCTGGAATCTGCA 60
DB 12 GAAAGATTTTGTGGCTCTCTTTTCTGAGACCTGCAATCTGGAATCTGCA 71
QY 61 CCAGGTGCAAAATGCTTTTAAAGTGAAGTATGATGCAACCTCTGGAGATAA 120
DB 72 CCAGGTGCAAAATGCTTTTAAAGTGAAGTATGATGCAACCTCTGGAGATAA 131
QY 121 GCATATGCTGGATACCAATGAAGATCTTTCAAGAGATGATCTTCTCATG 180
DB 132 GCATATGCTGGATACCAATGAAGATCTTTCAAGAGATGATCTTCTCATG 191
QY 181 AGAAATGCTCCCAACGAGAGACCAAGAAATTTCCAGTCTTCTGCAATGAAC 240
DB 192 AGAAATGCTCCCAACGAGAGACCAAGAAATTTCCAGTCTTCTGCAATGAAC 251
QY 241 CAGAGGTATCATTTGCTGTTTGTGTTACAGACCTTCAAAATATCAACCTTCTGCT 300
DB 252 CAGA-AGTATCATTTGCTGTTTGTGTTACAGACCTTCAAAATATCAACCTTCTGCT 310
QY 301 GTTGAATGTCATTCAGCCATTAAGATGAACAAAGACCGATCAACATGCTTTCTTA 360
DB 311 GTTGAATGTCATTCAGCCATTAAGATGAACAAAGACCGATCAACATGCTTTCTTA 370
QY 361 AATGACCAATCTGGAATTTTAAATTCCTTTCACACTTGCACCAACCAAGAGCCCA 420
DB 371 AATGACCAATCTGGAATTTTAAATTCCTTTCACACTTGCACCAACCAAGAGCCCA 430
QY 421 TCTGTCCTCATCTGGAATTTTAAATTCCTTTCACACTTGCACCAACCAAGAGCCCA 480
DB 431 TCTGTCCTCATCTGGAATTTTAAATTCCTTTCACACTTGCACCAACCAAGAGCCCA 490
QY 481 GCATATGATTTTATCAGGATCTGCAACGTAAGAAAGAAAGAAAGAAAGCAATTTGAA 540
DB 491 GCATATGATTTTATCAGGATCTGCAACGTAAGAAAGAAAGAAAGAAAGCAATTTGAA 550
QY 541 GTGATGAGCGCTGAAGATTAAGTGAAGAAAGAAAGAAAGAAAGCAATTTGCAATCCCTCT 600
DB 551 GTGATGAGCGCTGAAGATTAAGTGAAGAAAGAAAGAAAGAAAGCAATTTGCAATCCCTCT 610


```

Db      132 GCATATGCTGGGATACCAAGAAATACCTTCAAGCATGTAAGCTTCTCCATG 191
Qy      181 AGAAAAATTCACAGAGAGAGCAAGAAATTTCCCATGTCCTTCTTGCAATGTAAC 240
Db      192 AGAAAAATTCACAGAGAGAGCAAGAAATTTCCCATGTCCTTCTTGCAATGTAAC 251
Qy      241 CAGAGAGATCATCTGCTTGTGGTTGACAGACCTTCAAAAATATCACACCTTCTGCT 300
Db      252 CAGA-GGATATCTTGTGGTTGACAGACCTTCAAAAATATCACACCTTCTGCT 310
Qy      301 GTTGAAGTCAATCAGCCATTAAGATGAACAAAGAACCGGATCAACATGCTTTCTTA 360
Db      311 GTTGAAGTCAATCAGCCATTAAGATGAACAAAGAACCGGATCAACATGCTTTCTTA 370
Qy      361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCACTTGCAACCCCATGAGCCA 420
Db      371 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCACTTGCAACCCCATGAGCCA 430
Qy      421 TCTGAGCCCATCTGATTAATTAATTTGGTGGATATTTTGCATCATCAATGTCGAAT 480
Db      431 TCTGAGCCCATCTGATTAATTAATTTGGTGGATATTTTGCATCATCAATGTCGAAT 490
Qy      481 GCACACTGATTTTATCAGAGATCTGGCAACCTAGAGAGAGAGAGAGAGAGAGAGAG 540
Db      491 GCACACTGATTTTATCAGAGATCTGGCAACCTAGAGAGAGAGAGAGAGAGAGAGAG 550
Qy      541 GTGATGACGCTGGAAGATTAAGTGTGAAAAATGATGATCAATTTGAAAAATGCGAT 600
Db      551 GTGATGACGCTGGAAGATTAAGTGTGAAAAATGATGATCAATTTGAAAAATGCGAT 610
Qy      601 GATCCCTCTGAGACATGAAGAGG-GGGGATTAATTAAGATGCTTATGATGACAGAGATGAGAG 659
Db      611 GATCCCTCTGAGACATGAAGAGAGGCGATTAATTAAGATGCTTATGATGACAGAGATGAGAG 670
Qy      660 CTCAACCCCTCTCTGAAGGGCTGTGTCTGCTTCTCTCAAGAAATTAACATTTGTTCTG 719
Db      671 CTCAACCCCTCTCTGAAGGGCTGTGTCTGCTTCTCTCAAGAAATTAACATTTGTTCTG 730
Qy      720 TGTGATCTGTAGCATCTCTGAAGATTAACAGAGACATCAATTTTGTTCACCATCT 779
Db      731 TGTGATCTGTAGCATCTCTGAAGATTAACAGAGACATCAATTTTGTTCACCATCT 790
Qy      780 TCTTTTGTAAATTAATTTGAATGTGTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 839
Db      791 TCTTTTGTAAATTAATTTGAATGTGTCTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 850
Qy      840 CACCACTGAATCATTAAGCTATTCAGACTCAAAATATTTCTAAATATTTTCTGACGT 899
Db      851 CACCACTGAATCATTAAGCTATTCAGACTCAAAATATTTCTAAATATTTTCTGACGT 910
Qy      900 ATAGTGTAAATGTGTCTATGTGTATTTGTAAATTTGAAGCTTTTGAAGAT 959
Db      911 ATAGTGTAAATGTGTCTATGTGTATTTGTAAATTTGAAGCTTTTGAAGAT 970
Qy      960 AAGATCAGGCAATATGATATTTTCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1019
Db      971 AAGATCAGGCAATATGATATTTTCACTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1030
Qy      1020 AGTGAAGATATCAATTAATGATGTGAGAAATCATTTGAAGATGATCTTTTGAAGAT 1079
Db      1031 AGTGAAGATATCAATTAATGATGTGAGAAATCATTTGAAGATGATCTTTTGAAGAT 1090
Qy      1080 ACTTATATCACTCTGTATATGCTAAGTAAACAAAGAGAGAGAGAGAGAGAGAGAGAG 1139
Db      1091 ACTTATATCACTCTGTATATGCTAAGTAAACAAAGAGAGAGAGAGAGAGAGAGAGAG 1150
Qy      1140 ATGATTAATAATGAATTAATCATATATACAGGAGAGAGAGAGAGAGAGAGAGAGAG 1199
Db      1151 ATGATTAATAATGAATTAATCATATATACAGGAGAGAGAGAGAGAGAGAGAGAGAG 1210
Qy      1200 AGTTGATTAATATTTTCTGAATATCAGCCCTTAATGAGAGAGAGAGAGAGAGAGAG 1259

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Db      1211 AGTTGATTAATATTTTCTGAATATCAGCCCTTAATGAGAGAGAGAGAGAGAG 1270
Qy      1260 TTCTACAAATTTGTAAGAAGTCAATCTGTGCTAATTAATTAATTAATCAATCTTTT 1319
Db      1271 TTCTACAAATTTGTAAGAAGTCAATCTGTGCTAATTAATTAATTAATCAATCTTTT 1330
Qy      1320 TAAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTT 1345
Db      1331 AAAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTTAAAAATTTT 1356

RESULT 218
ADA40381
ID ADA40381 standard; cDNA; 1356 BP.
XX
AC ADA40381;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW Rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; neutrotic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerrary; cardiac; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PP 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 9; SEQ ID NO 763; 3205bp; English.
XX
XX
The invention relates to novel genes ADA39623-ADA40565 and proteins
ADA40566-ADA41501 for human secreted proteins, useful for preventing,
treating or ameliorating medical conditions e.g. by protein or gene
therapy. The polypeptides, nucleic acid molecules, antibodies or their
fragments, and agonists or antagonists that bind to the polypeptide are
useful for preparing a diagnostic or pharmaceutical composition for
diagnosing or treating cancer or other hyperproliferative disorder. The
polypeptides and nucleic acid molecules are also useful for detecting,
preventing, diagnosing, prognosticating, treating or ameliorating cancer
or other hyperproliferative disorders including neoplasms, autoimmune
disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
anaemia), haematopoietic or haematological disorders (e.g. anaemia,
thrombocytopenia), allergic reactions including asthma or eczema,
inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
Alzheimer's disease or Parkinson's disease), cardiovascular disorders
(e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
fungal or viral infections including HIV/AIDS), or wound healing and
disorders of epithelial cell proliferation. The nucleic acids are also

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CC useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from wipo at http://wipo.int/pub/publicated_pct_sequences.

CC Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 97.0%; Score 1305; DB 7; Length 1356;

Best Local Similarity 99.0%; Pred. No. 3.1e-254;

Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

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QY 1 GAAAGAAATGTTGGCTGCTCTTTTCTGAGCTGCACTTCACTGCTGAACCTGTGCA 60
DB 12 GAAAGAAATGTTGGCTGCTCTTTTCTGAGCTGCACTTCACTGCTGAACCTGTGCA 71
QY 61 CCAGGTCAGAAAATGCTTTTAAAGTGAAGCTTAACTGAAGAGCTGGAGATAAA 120
DB 72 CCAGGTCAGAAAATGCTTTTAAAGTGAAGCTTAACTGAAGAGCTGGAGATAAA 131
QY 121 GCATATGCTGGAGATCAATGAAGATACCTTCAAGAGATGTAGCTTTCTCATG 180
DB 132 GCATATGCTGGAGATCAATGAAGATACCTTCAAGAGATGTAGCTTTCTCATG 191
QY 181 AGAAAAGTCCCAAGAGAGCAAGCAAAATTTCCATGCTTCACTTTGCAATGAAC 240
DB 192 AGAAAAGTCCCAAGAGAGCAAGCAAAATTTCCATGCTTCACTTTGCAATGAAC 251
QY 241 CAGAGGGATCATTCGGTTGGTTGGTTAGACAGCCCTCAAAAATCAACCCCTCTGCT 300
DB 252 CAGAGGGATCATTCGGTTGGTTGGTTAGACAGCCCTCAAAAATCAACCCCTCTGCT 310
QY 301 GTTGAAGTGCATCAGCCATAGAAATGAAGCAAGAACCGATCAAAATGCTTTCTA 360
DB 311 GTTGAAGTGCATCAGCCATAGAAATGAAGCAAGAACCGATCAAAATGCTTTCTA 370
QY 361 AATGACCAAACTGTGAATTTTAAATCCCTTCCACATTTGCAACCACTGACCA 420
DB 371 AATGACCAAACTGTGAATTTTAAATCCCTTCCACATTTGCAACCACTGACCA 430
QY 421 TCTGTGCCATTCGGATTTATATTTGGTGAATTTTGGCATCATCATAGTGAAT 480
DB 431 TCTGTGCCATTCGGATTTATATTTGGTGAATTTTGGCATCATCATAGTGAAT 490
QY 481 GCACTACTGATTTTATCAGGATCTGCAAGTGAAGAAAGCAAAAGCAATCTGAA 540
DB 491 GCACTACTGATTTTATCAGGATCTGCAAGTGAAGAAAGCAAAAGCAATCTGAA 550
QY 541 GTGATGACCTGTAAGATTAAGTGAAGCAATGATCAATGAAATGGATCCCTCT 600
DB 551 GTGATGACCTGTAAGATTAAGTGAAGCAATGATCAATGAAATGGATCCCTCT 610
QY 601 GATCCCTGTAAGTGAAGGAGGCTGTTCTGCTTCAAGAAATTAACATTTGTTCTG 659
DB 611 GATCCCTGTAAGTGAAGGAGGCTGTTCTGCTTCAAGAAATTAACATTTGTTCTG 670
QY 660 CTCACCCCTCTGTAAGGAGGCTGTTCTGCTTCAAGAAATTAACATTTGTTCTG 719
DB 671 CTCACCCCTCTGTAAGGAGGCTGTTCTGCTTCAAGAAATTAACATTTGTTCTG 730
QY 720 TGTGATGCTGAGATCTGTAAGTGAAGCAAGAGATCATATATTTGTTCACTTCT 779
DB 731 TGTGATGCTGAGATCTGTAAGTGAAGCAAGAGATCATATATTTGTTCACTTCT 790
QY 780 TCTTTTGAATTAATTTGTAATGCTTGAAGTGAAGAAAGCAATTAATTAACCAACA 839
DB 791 TCTTTTGAATTAATTTGTAATGCTTGAAGTGAAGAAAGCAATTAATTAACCAACA 850
QY 840 CACCACTGAATCATTAAGCTATTCAGCACTCAAAATATCTTAAATATTTTCTGACGT 899

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DB 851 CACCACTGAATCATTAAGCTATTCAGCACTCAAAATATCTTAAATATTTTCTGACAGT 910
QY 900 ATAGTATTAATTAATGCTGATGATGATTTGATTTGATTTGATTTGATTTGATTTG 959
DB 911 ATAGTATTAATTAATGCTGATGATTTGATTTGATTTGATTTGATTTGATTTG 970
QY 960 AAGATGAGCATATGATTAATTTTCACTTCAAGAGCTTAAGCAAAATTAATTTTCC 1019
DB 971 AAGATGAGCATATGATTAATTTTCACTTCAAGAGCTTAAGCAAAATTAATTTTCC 1030
QY 1020 AGTGAAGATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTA 1079
DB 1031 AGTGAAGATTAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTA 1090
QY 1080 ACTATATCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1139
DB 1091 ACTATATCACTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1150
QY 1140 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1199
DB 1151 ATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1210
QY 1200 AGTTGATTAATTAATTTTCTGATTAATTAATTAATTAATTAATTAATTAAT 1259
DB 1211 AGTTGATTAATTAATTTTCTGATTAATTAATTAATTAATTAATTAATTAAT 1270
QY 1260 TTCTACAAATTTGTAAGTCCATCTGCTGCTAATTAATTAATTAATTAATTAAT 1319
DB 1271 TTCTACAAATTTGTAAGTCCATCTGCTGCTAATTAATTAATTAATTAATTAAT 1330
QY 1320 TAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1345
DB 1331 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1356

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RESULT 219

ADAL1594

ID ADAL1594 standard; DNA; 1356 BP.

XX AC ADAL1594;

DT 06-NOV-2003 (first entry)

XX Human cDNA encoding a novel secreted protein, SEQ ID NO 122.

XX cancer; inflammation; immune disorder; neurological disorder;

XX blood clotting disorder; food additive; food preservative;

XX storage capability; fat content; nutritional component; ds; gene; human.

XX Homo sapiens.

XX US200305236-A1.

XX 20-MAR-2003.

PF 14-MAR-2002; 2002US-00097065.

PR 18-DEC-1997; 97US-0068006P.

PR 18-DEC-1997; 97US-0068007P.

PR 18-DEC-1997; 97US-0068008P.

PR 18-DEC-1997; 97US-0068009P.

PR 18-DEC-1997; 97US-0068010P.

PR 18-DEC-1997; 97US-0068011P.

PR 18-DEC-1997; 97US-0068012P.

PR 18-DEC-1997; 97US-0068013P.

PR 18-DEC-1997; 97US-0068014P.

PR 18-DEC-1997; 97US-0068015P.

PA (HUMA-) HUMAN GENOME SCI INC.
 XX Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR;
 PI Kyaw H, Wei Y, Florence KA, Dunn DR, Florence C, Greene JM, Feng P;
 PI Ferrie AM, Yu G, Janat F, Ni J;
 XX WPI: 2003-567105/53.
 DR P-PSDB: ADA11718.
 XX
 PT New secreted HKABT24 nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 XX
 PS Claim 1; SEQ ID NO 122; 118bp; English.
 CC The invention relates to an isolated HKABT24 nucleic acid molecule. The
 CC polypeptides, nucleic acids and antibodies are useful for diagnosing a
 CC pathological condition or a susceptibility to a pathological condition,
 CC for preventing, treating, or ameliorating a medical condition, such as
 CC cancer, inflammation and other immune disorders, neurological and blood
 CC clotting disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
 CC antagonist may also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present sequence represents cDNA encoding a
 CC novel human secreted protein. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov.uk/sequence.html?DocID=20030055236.
 XX
 SQ Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;
 Query Match 97.0%; Score 1305; DB 8; Length 1356;
 Best Local Similarity 99.0%; Pred. No. 3.1e-254;
 Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

DB 491 GCACTACTGATTTTATACAGGATCTGCAACGTAGAAAGAAACAAAGAACATCTGAA 550
 QY 541 GTGATGACGCTGGAAGATTAAGTGAAGAAATGATCAATGAAATGGCATCCCTCT 600
 DB 551 GTGATGACGCTGGAAGATTAAGTGAAGAAATGATCAATGAAATGGCATCCCTCT 610
 QY 601 GATCCCTGGAATGAAGG-GGGGATTAATGAATGCTTCATGACAGAGATGAGAG 659
 DB 611 GATCCCTGGAATGAAGGAGGAGATTAATGAATGCTTCATGACAGAGATGAGAG 670
 QY 660 CTACCCCTCTGGAAGGCTGTTGTTGCTTCTGAAAGAAATTAACATTTGTTCTG 719
 DB 671 CTACCCCTCTGGAAGGCTGTTGTTGCTTCTGAAAGAAATTAACATTTGTTCTG 730
 QY 720 TGTGACTGTGAGCATCCGGAATATCAAGAGAGATCATATTTGTTCAACATCT 779
 DB 731 TGTGACTGTGAGCATCCGGAATATCAAGAGAGATCATATTTGTTCAACATCT 790
 QY 780 TCTTTTGTATTAATTTTGAATGTGCTTGAAGTGAAGAAAGCAATTAATACCA 839
 DB 791 TCTTTTGTATTAATTTTGAATGTGCTTGAAGTGAAGAAAGCAATTAATACCA 850
 QY 840 CACCACTGAATCATTAAGCTATTCAGACTGAAATATTTCTTAATTTTCTGACGT 899
 DB 851 CACCACTGAATCATTAAGCTATTCAGACTGAAATATTTCTTAATTTTCTGACGT 910
 QY 900 ATAGGTATTAATGTGCTATGTGATTTGATGATTAATGATTAATGATTTTGA 959
 DB 911 ATAGGTATTAATGTGCTATGTGATTTGATGATTAATGATTAATGATTTTGA 970
 QY 960 AAGATCAGGATATGATTAATTTTCACTTCAAGAACTTAAGGAAATTAATTTTC 1019
 DB 971 AAGATCAGGATATGATTAATTTTCACTTCAAGAACTTAAGGAAATTAATTTTC 1030
 QY 1020 AGTGAAGATTAATTAATGATTAATGATTAATGATTAATGATTTTGAAGATC 1079
 DB 1031 AGTGAAGATTAATTAATGATTAATGATTAATGATTAATGATTTTGAAGATC 1090
 QY 1080 ACTTATACCTCTGTATGATTAATGATTAATGATTAATGATTTTGAAGATC 1139
 DB 1091 ACTTATACCTCTGTATGATTAATGATTAATGATTAATGATTTTGAAGATC 1150
 QY 1140 ATGATTAATTAATGATTAATGATTAATGATTAATGATTTTGAAGATC 1199
 DB 1151 ATGATTAATTAATGATTAATGATTAATGATTAATGATTTTGAAGATC 1210
 QY 1200 AGTGAATTAATTAATGATTAATGATTAATGATTTTGAAGATC 1259
 DB 1211 AGTGAATTAATTAATGATTAATGATTAATGATTTTGAAGATC 1270
 QY 1260 TTCTCAATTTTGTAAAGTCCAAATCTGCTAATTAATTAATTAATTAATTAAT 1319
 DB 1271 TTCTCAATTTTGTAAAGTCCAAATCTGCTAATTAATTAATTAATTAATTAAT 1330
 QY 1320 TAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1345
 DB 1331 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1356

RESULT 220
 ADD37752
 ID ADD37752 standard; cDNA; 1356 BP.
 XX
 AC ADD37752;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 XX Human secreted protein encoding sequence #234.
 DX human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
 XX

OS Homo sapiens.
XX
PN MO200290526-A2.
XX
PD 14-NOV-2002.
XX
PF 19-MAR-2002; 2002MO-US008279.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
XX
XX WPI; 2003-140218/13.
XX
XX New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing or
PT treating allergic or autoimmune disorders, or related immediate
PT hypersensitivity disorders.
XX
XX Claim 7; SEQ ID NO 234; 1323bp; English.
XX
XX The present invention relates to an isolated polypeptide or human
CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
CC their fragments, and agonists or antagonists that bind are useful for
CC preparing a diagnostic or pharmaceutical composition for diagnosing or
CC treating allergic or autoimmune disorders. The polypeptide is also useful
CC for identifying a binding partner by contacting the polypeptide with a
CC binding partner and determining whether the binding partner increases or
CC decreases the activity of the polypeptide. The polypeptides and nucleic
CC acid molecules are also useful for detecting, preventing, diagnosing,
CC prognosticating, treating or ameliorating inflammatory disorders
CC neoplastic diseases, wound healing and disorders of epithelial cell
CC proliferation, immune disorders, cardiovascular disorders, blood-related
CC disorders, infectious diseases, endocrine disorders, or gastrointestinal
CC disorders. The nucleic acids are also useful for chromosome
CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein encoding sequence.
XX
XX Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;
SQ
Query Match 97.0%; Score 1305; DB 9; Length 1356;
Best Local Similarity 99.0%; Pred. No. 3.1e-254;
Matches 1333; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
QY 1 GAAAGAAATGTTGGCTCTCTTTTCTGAGCTGGCATTGCTGAACCTCTGCA 60
DB 12 GAAAGAAATGTTGGCTCTCTTTTCTGAGCTGGCATTGCTGAACCTCTGCA 71
QY 61 CCAAGTCCAGAAATGCTTTTAAAGTAGATAGTATCAGAACGCTCTGGAGATATA 120
DB 72 CCAAGTCCAGAAATGCTTTTAAAGTAGATAGTATCAGAACGCTCTGGAGATATA 131
QY 121 GCATATGCTGGATCCCAATGAAGATACCTTCAAGGATGGTAGCTTCTCCATG 180
DB 132 GCATATGCTGGATCCCAATGAAGATACCTTCAAGGATGGTAGCTTCTCCATG 191
QY 181 AGAAAGATCCCAAGAGAGCAAGAAATTTCCATGCTCACTTGGCAATGTAAAC 240
DB 192 AGAAAGATCCCAAGAGAGCAAGAAATTTCCATGCTCACTTGGCAATGTAAAC 251
QY 241 CAGAGGATATCTTGGTTGGTTGATACAGACCTTCAAAAATCAGACCTTCTGCT 300
DB 252 CAGAGGATATCTTGGTTGGTTGATACAGACCTTCAAAAATCAGACCTTCTGCT 310
QY 301 GTTAGAGTGCATGAGCATTAAGATGAACAAAGACGATCAACATGCTTCTTCTA 360

DB 311 GTTAGAGTGCATGAGCATTAAGATGAACAAAGACGATCAACATGCTTCTTCTA 370
QY 361 AATGACCAACTCTGGAATTTTAAATTCCTTCCACACTTGCACACCCATGACCA 420
DB 371 AATGACCAACTCTGGAATTTTAAATTCCTTCCACACTTGCACACCCATGACCA 430
QY 421 TCTGAGCCCATCTGGAATTTTAAATTCCTTCCACACTTGCACACCCATGACCA 480
DB 431 TCTGAGCCCATCTGGAATTTTAAATTCCTTCCACACTTGCACACCCATGACCA 490
QY 481 GCACTACTGATTTTATCAAGGATCTGCAACCTGAGAGAGAGAGAGAGAGAGAG 540
DB 491 GCACTACTGATTTTATCAAGGATCTGCAACCTGAGAGAGAGAGAGAGAGAGAG 550
QY 541 GTGATGACGCTGGAAGATTAAGTGTGAAAACATATCACAATTTGAAATGCAAT 600
DB 551 GTGATGACGCTGGAAGATTAAGTGTGAAAACATATCACAATTTGAAATGCAAT 610
QY 601 GATCCCTGGAATGAGAGG-GGGCATTTATGATGCTTCTCAAGAAATTAACATTT 659
DB 611 GATCCCTGGAATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 670
QY 660 CTCACCCCTCTCTGAGAGGCTGTGTCTGCTTCTCTCAAGAAATTAACATTT 719
DB 671 CTCACCCCTCTCTGAGAGGCTGTGTCTGCTTCTCTCAAGAAATTAACATTT 730
QY 720 TGTGATCTGAGCATCTGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 779
DB 731 TGTGATCTGAGCATCTGGAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 790
QY 780 TCTTTTGAATTAATTTTGAATTTGAAATGCTGAAAGTGAAGAGAGAGAGAGAG 839
DB 791 TCTTTTGAATTAATTTTGAATTTGAAATGCTGAAAGTGAAGAGAGAGAGAGAG 850
QY 840 CACCACTGAATTCATTAAGCTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 899
DB 851 CACCACTGAATTCATTAAGCTATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 910
QY 900 ATAGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 959
DB 911 ATAGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 970
QY 960 AAGATCAGGATTAATTTTCAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1019
DB 971 AAGATCAGGATTAATTTTCAACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 1030
QY 1020 AGTGAGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1079
DB 1031 AGTGAGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1090
QY 1080 ACTTATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1139
DB 1091 ACTTATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
QY 1140 ATGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1199
DB 1151 ATGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1210
QY 1200 AGTGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1259
DB 1211 AGTGATTAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270
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DB 1271 TTCTTCAATTTTGAATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1330
QY 1320 TAAAAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 1345
DB 1331 TAAAAAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAATTTTGAAT 1356

Tue Jun 8 07:15:34 2004

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Page 348

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 2280998010 residues

Total number of hits satisfying chosen parameters: 516

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%

Maximum Match 100%
Listing first 65000 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCR_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/PCRUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1346	100.0	1346	9	US-09-989-722-386
2	1346	100.0	1346	9	US-09-989-723-386
3	1346	100.0	1346	9	US-09-989-729-386
4	1346	100.0	1346	9	US-09-989-727-386
5	1346	100.0	1346	9	US-09-989-731-386
6	1346	100.0	1346	9	US-09-989-732-386
7	1346	100.0	1346	9	US-09-991-073-386
8	1346	100.0	1346	9	US-09-990-442-386
9	1346	100.0	1346	9	US-09-991-163-386
10	1346	100.0	1346	9	US-09-993-604-386
11	1346	100.0	1346	9	US-09-990-456-386
12	1346	100.0	1346	9	US-09-989-721-386
13	1346	100.0	1346	9	US-09-992-598-386
14	1346	100.0	1346	9	US-09-989-733A-386

15	1346	100.0	1346	9	US-09-989-735-386	Sequence 386, App
16	1346	100.0	1346	9	US-09-990-444-386	Sequence 386, App
17	1346	100.0	1346	9	US-09-991-181-386	Sequence 386, App
18	1346	100.0	1346	9	US-09-989-730-386	Sequence 386, App
19	1346	100.0	1346	9	US-09-990-436-386	Sequence 386, App
20	1346	100.0	1346	9	US-09-993-687-386	Sequence 386, App
21	1346	100.0	1346	10	US-09-989-734-386	Sequence 386, App
22	1346	100.0	1346	10	US-09-997-653-386	Sequence 386, App
23	1346	100.0	1346	10	US-09-993-667-386	Sequence 386, App
24	1346	100.0	1346	10	US-09-997-428-386	Sequence 386, App
25	1346	100.0	1346	10	US-09-997-666-386	Sequence 386, App
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27	1346	100.0	1346	10	US-09-990-562-386	Sequence 386, App
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64	1346	100.0	1346	11	US-09-989-733-386	Sequence 386, App
65	1346	100.0	1346	11	US-09-992-643-386	Sequence 386, App
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84	1346	100.0	1346	13	US-10-142-886-481	Sequence 481, App
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237	1346	100.0	1346	15	US-10-153-934-481	Sequence 481, App	310	1346	100.0	1346	15	US-10-143-091-481	Sequence 481, App
238	1346	100.0	1346	15	US-10-140-807-481	Sequence 481, App	311	1346	100.0	1346	15	US-10-145-629-481	Sequence 481, App
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389	1346	100.0	1346	15	US-10-146-750-481	Sequence 481, App	462	1346	100.0	1346	16	US-10-142-429-481	Sequence 481, App
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397	1346	100.0	1346	15	US-10-123-109-481	Sequence 481, App	470	1346	100.0	1346	16	US-10-145-871-481	Sequence 481, App
398	1346	100.0	1346	15	US-10-123-154-481	Sequence 481, App	471	1346	100.0	1346	16	US-10-145-871-481	Sequence 481, App
399	1346	100.0	1346	15	US-10-123-157-481	Sequence 481, App	472	1346	100.0	1346	16	US-10-145-878-481	Sequence 481, App
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405	1346	100.0	1346	15	US-10-125-927-481	Sequence 481, App	478	1346	100.0	1346	16	US-10-152-376-481	Sequence 481, App
406	1346	100.0	1346	15	US-10-142-889-481	Sequence 481, App	479	1346	100.0	1346	16	US-10-152-381-481	Sequence 481, App
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414	1346	100.0	1346	15	US-10-152-391-481	Sequence 481, App	487	1346	100.0	1346	16	US-10-158-789-481	Sequence 481, App
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417	1346	100.0	1346	15	US-10-157-785-481	Sequence 481, App	490	1346	100.0	1346	16	US-10-140-020-481	Sequence 481, App
418	1346	100.0	1346	15	US-10-157-794-481	Sequence 481, App	491	1346	100.0	1346	16	US-10-140-023-481	Sequence 481, App
419	1346	100.0	1346	15	US-10-157-796-481	Sequence 481, App	492	1346	100.0	1346	16	US-10-140-809-481	Sequence 481, App
420	1346	100.0	1346	15	US-10-160-500-481	Sequence 481, App	493	1346	100.0	1346	16	US-10-140-865-481	Sequence 481, App
421	1346	100.0	1346	15	US-10-121-046-481	Sequence 481, App	494	1346	100.0	1346	16	US-10-141-701-481	Sequence 481, App
422	1346	100.0	1346	15	US-10-123-116-481	Sequence 481, App	495	1346	100.0	1346	16	US-10-141-760-481	Sequence 481, App
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435	1346	100.0	1346	15	US-10-156-846-481	Sequence 481, App	508	1346	100.0	1346	16	US-10-140-527-481	Sequence 481, App
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449	1346	100.0	1346	15	US-10-125-932-481	Sequence 481, App							
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451	1346	100.0	1346	16	US-10-137-867-481	Sequence 481, App							
452	1346	100.0	1346	16	US-10-140-473-481	Sequence 481, App							

ALIGNMENTS

RESULT 1
US-09-989-722-386
; Sequence 386, Application US/09989722
; Patent No. US20020072067A1


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; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-128-692A-481

Query Match      100.0%; Score 1346; DB 16; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1.4e-295;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAAGAATGTTGGCTGCTCTTTTCTGTGATCGCCATTCAGCTGAACTCTGTCA 60
Db 1 GAAGAATGTTGGCTGCTCTTTTCTGTGATCGCCATTCAGCTGAACTCTGTCA 60

Qy 61 CCAGGTGAGAAATGCTTTTAAAGTGAAGCTTATGAGAAAGCTCTGGAGATAA 120
Db 61 CCAGGTGAGAAATGCTTTTAAAGTGAAGCTTATGAGAAAGCTCTGGAGATAA 120

Qy 121 GCATATGCTGGATACCAATGAAGATACCTCTCAAGCGATGATGCTTCTCAAG 180
Db 121 GCATATGCTGGATACCAATGAAGATACCTCTCAAGCGATGATGCTTCTCAAG 180

Qy 181 AGAAAGTTCCTCAACAGAGAGCAAGAAATTTCCCATGTCCTATGCAATGTAAC 240
Db 181 AGAAAGTTCCTCAACAGAGAGCAAGAAATTTCCCATGTCCTATGCAATGTAAC 240

Qy 241 CAGAGGGATCATCTGTTGTGTGTTACAGACCCCTCAAAAATCAACCCCTCTGCT 300
Db 241 CAGAGGGATCATCTGTTGTGTGTTACAGACCCCTCAAAAATCAACCCCTCTGCT 300

Qy 301 GTTGAAGTGCATACGACCATTAAGATGAACAGAAACCGATCAACATGCTTCTTCTA 360
Db 301 GTTGAAGTGCATACGACCATTAAGATGAACAGAAACCGATCAACATGCTTCTTCTA 360

Qy 361 AATGACCAACTCTGGAATTTTAAATTCCTTCCACACTTGACACCCATGACCA 420
Db 361 AATGACCAACTCTGGAATTTTAAATTCCTTCCACACTTGACACCCATGACCA 420

Qy 421 TCTGTGCCCATCTGATATATATATTTGGTGTGATATTTGATCAATGATGCAAT 480
Db 421 TCTGTGCCCATCTGATATATATATTTGGTGTGATATTTGATCAATGATGCAAT 480

Qy 481 GCATCTACTGATTTTATACAGGATCTGCAACGTAGAGAAAGAAAGAAACCATCTGAA 540
Db 481 GCATCTACTGATTTTATACAGGATCTGCAACGTAGAGAAAGAAAGAAACCATCTGAA 540

Qy 541 GTGATGACGCTGAAGATPAAGTGTAAACCATGATCAATGAAATGCAATCCCTCT 600
Db 541 GTGATGACGCTGAAGATPAAGTGTAAACCATGATCAATGAAATGCAATCCCTCT 600

Qy 601 GATCCCTGAGCANTAAAGGGGGGCAATTAATGAAGCTTCATGACAGAGGATGAGG 660
Db 601 GATCCCTGAGCANTAAAGGGGGGCAATTAATGAAGCTTCATGACAGAGGATGAGG 660

Qy 661 TCACCCCTCTCTGAAGGGCTGTGTTGCTCTCTCAAGAAATTAACATTTGTTCTGT 720
Db 661 TCACCCCTCTCTGAAGGGCTGTGTTGCTCTCTCAAGAAATTAACATTTGTTCTGT 720

Qy 721 GTGATGCTGAGCATCTGAAATACCAAGAGCATATATATTTGTTCAACTTCTT 780
Db 721 GTGATGCTGAGCATCTGAAATACCAAGAGCATATATATTTGTTCAACTTCTT 780

Qy 781 CTTTGTGATTAATTTTGAATGTGCTTGAAGTGAAGGAAATCAATTAACCAAC 840
Db 781 CTTTGTGATTAATTTTGAATGTGCTTGAAGTGAAGGAAATCAATTAACCAAC 840
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Qy 841 ACCACTGAATATATAGCTATTCAGACTCAAAATATTTTAAATTTTCTGACAGTA 900
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Qy 901 TAGGTATTAATATGTCATGATGATTTAGTATTTAGTATTAAGCATTTTGAAGATA 960
Db 901 TAGGTATTAATATGTCATGATGATTTAGTATTTAGTATTTAGCATTTTGAAGATA 960

Qy 961 AGATCAGGATATATATATATTTTCAACTTCAAGAGCTTAAGAGAAATTAATTTTCA 1020
Db 961 AGATCAGGATATATATATATTTTCAACTTCAAGAGCTTAAGAGAAATTAATTTTCA 1020

Qy 1021 GTGAGAAATACATATATATATATGATGATGATGATGATGATGATGATGATGAT 1080
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Qy 1081 CTTATATCACTCTGATATATGATGATGATGATGATGATGATGATGATGATGAT 1140
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Qy 1141 TGGATTAATAATGATTAATCTCATATACAGGATGATGATGATGATGATGATGATGAT 1200
Db 1141 TGGATTAATAATGATTAATCTCATATACAGGATGATGATGATGATGATGATGATGAT 1200

Qy 1201 GTTGAATATATATTTTCTGAATATACGCTTAAATGAGCAATTTGATTTGTACAT 1260
Db 1201 GTTGAATATATATTTTCTGAATATACGCTTAAATGAGCAATTTGATTTGTACAT 1260

Qy 1261 TCTACATTTTGTAAAGTCCATGCTGCTACTTATTAAGTATTAATCACTCTTCTT 1320
Db 1261 TCTACATTTTGTAAAGTCCATGCTGCTACTTATTAAGTATTAATCACTCTTCTT 1320

Qy 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
Db 1321 AAAAAAAAAAAAAAAAAAAAAA 1346
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RESULT 508

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US-10-140-927-481
; Sequence 481, Application US/10140927
; Publication No. US20040009548A1
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GENERAL INFORMATION:

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; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C180
; CURRENT APPLICATION NUMBER: US/10/140,927
; PRIORITY FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-927-481
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Query Match 100.0%; Score 1346; DB 16; Length 1346;

Best Local Similarity 100.0%; Pred. No. 1.4e-295;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GAAGAATGTTGTGGCTCTTTTTCCTGGTACCTGTCAC	60
Qy	61	CCAGGTGCAGAAATGCTTTTAAAGTGAAGCTTATGAAACAGCTCTGGGAGATPAA	120
Db	61	CCAGGTGCAGAAATGCTTTTAAAGTGAAGCTTATGAAACAGCTCTGGGAGATPAA	120
Qy	121	GCATATGCTTGGATATCCATGAAGAAATACCTTCAAGAGATGATAGCTTCTGCATG	180
Db	121	GCATATGCTTGGATATCCATGAAGAAATACCTTCAAGAGATGATAGCTTCTGCATG	180
Qy	181	AGAAAAGTTCCTCCACAGAGAGCAAGAAATTTCCATGTCCTACTTTGCAATGTAAAC	240
Db	181	AGAAAAGTTCCTCCACAGAGAGCAAGAAATTTCCATGTCCTACTTTGCAATGTAAAC	240
Qy	241	CAGAGGGATCATTTCTGGTTGTGGTTACAGACCCTTCAAAATAACACCCCTCTGCT	300
Db	241	CAGAGGGATCATTTCTGGTTGTGGTTACAGACCCTTCAAAATAACACCCCTCTGCT	300
Qy	301	GTTAGGTGCATCAGCCATAAGATGAATGAACAAGACGGATCAACATGCTCTTCTTA	360
Db	301	GTTAGGTGCATCAGCCATAAGATGAATGAACAAGACGGATCAACATGCTCTTCTTA	360
Qy	361	AATGACCAAACTCTGGAATTTTAAATATCCCTTCACATTCGACCAACCATGGAACCA	420
Db	361	AATGACCAAACTCTGGAATTTTAAATATCCCTTCACATTCGACCAACCATGGAACCA	420
Qy	421	TCGTGCCATCTGGAATTAATATTTGGTGAATTTTGCATCATCATAGTTGCAAT	480
Db	421	TCGTGCCATCTGGAATTAATATTTGGTGAATTTTGCATCATCATAGTTGCAAT	480
Qy	481	GCATCTACGATTTTATACAGGGATCTGGCAAGTATGAAGAAAGCAAAAGAACCATCTGAA	540
Db	481	GCATCTACGATTTTATACAGGGATCTGGCAAGTATGAAGAAAGCAAAAGAACCATCTGAA	540
Qy	541	GTGATGACGCTGAAGATTAAGTGTGAACATGATCACAATTGAATAATGGATCCCTCT	600
Db	541	GTGATGACGCTGAAGATTAAGTGTGAACATGATCACAATTGAATAATGGATCCCTCT	600
Qy	601	GATCCCTCTGACATGAAGGGGGCAATTAATGATGCTTCAATGACAGAGATGAAGGC	660
Db	601	GATCCCTCTGACATGAAGGGGGCAATTAATGATGCTTCAATGACAGAGATGAAGGC	660
Qy	661	TCAACCCCTCTGAAAGGCTGTGTTCTGCTTCCAGAAATTPAACTATGTTCTGT	720
Db	661	TCAACCCCTCTGAAAGGCTGTGTTCTGCTTCCAGAAATTPAACTATGTTCTGT	720
Qy	721	GTGATGCTGAGCATCTGAATAACCAAGAGCATCATATTTTGTTCACCATCTT	780
Db	721	GTGATGCTGAGCATCTGAATAACCAAGAGCATCATATTTTGTTCACCATCTT	780
Qy	781	CTTTGTATAAATTTTGAATGTCTTGAAGTGAAGCAATCAATTAACCAACAC	840
Db	781	CTTTGTATAAATTTTGAATGTCTTGAAGTGAAGCAATCAATTAACCAACAC	840
Qy	841	ACCATGAATCATATAGCTATTTCAACGATCAAAATATTTCTAATAATTTTCTGACGTA	900
Db	841	ACCATGAATCATATAGCTATTTCAACGATCAAAATATTTCTAATAATTTTCTGACGTA	900
Qy	901	TAGTGTATAAATGTGCTATGTGATTTTGTATGTAATGATTTTGAAGCAATTTTGAATA	960
Db	901	TAGTGTATAAATGTGCTATGTGATTTTGTATGTAATGATTTTGAAGCAATTTTGAATA	960
Qy	961	AGATCAGGCATATGTATATTTTCAACTCAAGACCTTAAGGAAAAATTAATTTTCCA	1020
Db	961	AGATCAGGCATATGTATATTTTCAACTCAAGACCTTAAGGAAAAATTAATTTTCCA	1020
Qy	1021	GTGAGAAATCATATATATGTGTTGAATACTTGAATAAGATCCTTTTGAACATCA	1080
Db	1021	GTGAGAAATCATATATATGTGTTGAATACTTGAATAAGATCCTTTTGAACATCA	1080

[illegible]

RESULT 509

US-10-14/-536-461
; Sequence 481, Application US/10147536
; Publication No. US20040077064A1

GENERAL INFORMATION:

```

1  APPLICANT: Baker, Kevin P.
2  APPLICANT: Beresini, Maureen
3  APPLICANT: DeForge, Laura
4  APPLICANT: Desnoyers, Inc
5  APPLICANT: Filvaroff, Ellen
6  APPLICANT: Gao, Wei-Qiang
7  APPLICANT: Gerritsen, Mary E.
8  APPLICANT: Goddard, Audrey
9  APPLICANT: Godowski, Paul J.
10 APPLICANT: Gurney, Austin L.
11 APPLICANT: Sherwood, Steven
12 APPLICANT: Smith, Victoria
13 APPLICANT: Stewart, Timothy A.
14 APPLICANT: Tumas, Daniel
15 APPLICANT: Watanabe, Collin K
16 APPLICANT: Wood, William
17
18 APPLICANT: Zhang, Zemin
19
20 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
21 FILE REFERENCE: P33081C349
22
23 CURRENT APPLICATION NUMBER: US/10/147,536
24
25 PRIOR APPLICATION REMOVED: 2002-05-17
26
27 NUMBER OF SEQ ID NOS: 550
28
29 SEQ ID NO 481
30
31 LENGTH: 1346
32
33 TYPE: DNA
34
35 ORGANISM: Homo Sapien
36
37 US-10-147-536--481

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Query Match	Score	DB	Length
100.0%	1346	17	1346

Best Local Similarity 100.0%; Pred. No. 1.4e-295;
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GAAAGAAATGTGTGGCTCTCTTTTCTGGTGACTGCCATTCAATGCAACTGTCAAA	60
Db	1	GAAAGAAATGTGTGGCTCTCTTTTCTGGTGACTGCCATTCAATGCAACTGTCAAA	60
QY	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAAGTCTGATCAGAAACACTCTGGAGATTA	120
Db	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAAGTCTGATCAGAAACACTCTGGAGATTA	120
QY	121	GCATATGCTGGGATCCAAATGAAGAAATCCTCTTCAAGGAGTGTAGCTTTCCTCAATG	180
Db	121	GCATATGCTGGGATCCAAATGAAGAAATCCTCTTCAAGGAGTGTAGCTTTCCTCAATG	180

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QY 181 AGAAAGTTCACAGAGAGCAAGAAATTCCTGCTCTTGTGCAATGTAAC 240
DB 181 AGAAAGTTCACAGAGAGCAAGAAATTCCTGCTCTTGTGCAATGTAAC 240
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DB 241 CAGAGGATCATTTGGTTGGTTACAGCCCTTCAAAAATCAACCCCTTCTGT 300
QY 301 GTTGAAGTCAATGACCATAGAAAGAAACCGGATCAAGATGCTTTCTTCTA 360
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QY 361 AATGACCAAACTCTGAAATTTTAAAAATCCCTTCACACTTGACCAACCAAGACCA 420
DB 361 AATGACCAAACTCTGAAATTTTAAAAATCCCTTCACACTTGACCAACCAAGACCA 420
QY 421 TCTGTGCCATCTGATTAATTAATTTGGTGTGATATTTTGCATCATATGTCATTT 480
DB 421 TCTGTGCCATCTGATTAATTAATTTGGTGTGATATTTTGCATCATATGTCATTT 480
QY 481 GCACATCAATTTTATTCAGGATCTGCAACCTAAGAAAGAAACCAATCTGAA 540
DB 481 GCACATCAATTTTATTCAGGATCTGCAACCTAAGAAAGAAACCAATCTGAA 540
QY 541 GTGATGACGCTGAAGATTAAGTGTGAAACATGATCATCAATTTGAAATGCAATCCCTCT 600
DB 541 GTGATGACGCTGAAGATTAAGTGTGAAACATGATCATCAATTTGAAATGCAATCCCTCT 600
QY 601 GATCCCTCTGACATGAGGGGGGCAATTAATGATGATCTTCATGACAGAGATGAGAGGC 660
DB 601 GATCCCTCTGACATGAGGGGGGCAATTAATGATGATCTTCATGACAGAGATGAGAGGC 660
QY 661 TCACCCCTCTGAGAGGGGCTGTGTTCTGCTCCAGAAATTAACAATTTGTTCTGT 720
DB 661 TCACCCCTCTGAGAGGGGCTGTGTTCTGCTCCAGAAATTAACAATTTGTTCTGT 720
QY 721 GTGACGCTGAGCATCTGAAATACCAAGACAGATCATATTTTGTTCACATTTCT 780
DB 721 GTGACGCTGAGCATCTGAAATACCAAGACAGATCATATTTTGTTCACATTTCT 780
QY 781 CTTTGTGATTAATTTGATGATGCTTGAAGTGAAGCAATCATTAATCCCAAC 840
DB 781 CTTTGTGATTAATTTGATGATGCTTGAAGTGAAGCAATCATTAATCCCAAC 840
QY 841 ACCATGAAATCATPAAGTATTCAGACTCAAAAATCTAATAATTTTCTGACAGTA 900
DB 841 ACCATGAAATCATPAAGTATTCAGACTCAAAAATCTAATAATTTTCTGACAGTA 900
QY 901 TAGATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
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DB 1021 GTGAGAAATCATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1081 CTTATATCACTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
DB 1081 CTTATATCACTCTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 TGGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 TGGATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 GTTGAATTAATTTTGTGATATCAAGCCCTAATAGGCAATCTATTTGTGACATTT 1260
DB 1201 GTTGAATTAATTTTGTGATATCAAGCCCTAATAGGCAATCTATTTGTGACATTT 1260

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QY 1261 TCTACATTTGTAAGAGTCCATCTGTGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
DB 1261 TCTACATTTGTAAGAGTCCATCTGTGCTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
QY 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346
DB 1321 AAAAAAAAAAAAAAAAAAAAAAAAAA 1346

RESULT 510
US-10-372-876-17
; Sequence 17, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021p1
; CURRENT APPLICATION NUMBER: US/10/372, 876
; PRIOR FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patemlin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-372-876-17

Query Match 98.5%; Score 1325.4; DB 13; Length 1432;
Best Local Similarity 99.5%; Pred. No. 76-291;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 GAAAGATGTTGGCTGCTCTTTTGTGAGTCCATTCATGCTGAACCTCTGTCAA 60
DB 63 GAAAGATGTTGGCTGCTCTTTTGTGAGTCCATTCATGCTGAACCTCTGTCAA 122
QY 61 CCAAGTGCAGAAAGCTTTTAAAGTGAAGTCTTAGTCAAGAAAGCTGTGGAGATAAA 120
DB 123 CCAAGTGCAGAAAGCTTTTAAAGTGAAGTCTTAGTCAAGAAAGCTGTGGAGATAAA 182
QY 121 GCATATGCTGGATACCAATGAGATTAACCTCTTCAAGAGCATGATGCTTTCTTCATG 180
DB 183 GCATATGCTGGATACCAATGAGATTAACCTCTTCAAGAGCATGATGCTTTCTTCATG 242
QY 181 AGAAAGTTCACAGAGAGCAAGAAATTTCCATGTCTTCTTGTGCAATGTAAC 240
DB 243 AGAAAGTTCACAGAGAGCAAGAAATTTCCATGTCTTCTTGTGCAATGTAAC 302
QY 241 CAGAGGATCATTTGGTTGGTTACAGCCCTTCAAAAATCAACCCCTTCTGT 300
DB 303 CAGAGGATCATTTGGTTGGTTACAGCCCTTCAAAAATCAACCCCTTCTGT 362
QY 301 GTTGAAGTCAATGACCATAGAAAGAAACCGGATCAAGATGCTTTCTTCTA 360

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Db 363 GTTGAAGTCAATCAGCCATTAAGAAAGAAACCGGATCAACATGCTCTTCTA 422
Qy 361 AATGACCAATCTGGAATTTTAAATCCCTTCCACATCTGACCAACCCATGAGCCCA 420
Db 423 AATGACCAATCTGGAATTTTAAATCCCTTCCACATCTGACCAACCCATGAGCCCA 482
Qy 421 TCTGTCCTCATGATTAATTAATTTGATGATTAATTTGATGATTAATTTGATGAT 480
Db 483 TCTGTCCTCATGATTAATTAATTTGATGATTAATTTGATGATTAATTTGATGAT 542
Qy 481 GCACTAATGATTTTCAAGGATCTGCAACGTAAGAAAGAAAGAAAGAAAGAAAG 540
Db 543 GCACTAATGATTTTCAAGGATCTGCAACGTAAGAAAGAAAGAAAGAAAGAAAG 602
Qy 541 GTGATGAGCTGTAAGATTAAGTGAAGAAAGAAAGAAAGAAAGAAAGAAAG 600
Db 603 GTGATGAGCTGTAAGATTAAGTGAAGAAAGAAAGAAAGAAAGAAAGAAAG 662
Qy 601 GATCCCTGGAAGAGG-GGGCAATTAATGATGATGATGATGATGATGATGATG 659
Db 663 GATCCCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Qy 660 CTCACCCCTCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 719
Db 723 CTCACCCCTCTGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 782
Qy 720 TGTGATGCTGAGACATCCGGAATTAACAAAGAGAGAGAGAGAGAGAGAGAGAG 779
Db 783 TGTGATGCTGAGACATCCGGAATTAACAAAGAGAGAGAGAGAGAGAGAGAG 842
Qy 780 TCTTTTGTATAATTTTGAATGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 839
Db 843 TCTTTTGTATAATTTTGAATGCTGGAAGAGAGAGAGAGAGAGAGAGAGAGAG 902
Qy 840 CACCACTGAAATCATTAAGCTATTCAAGACTCAAAATTTCTAAATTTTCTGACAGT 899
Db 903 CACCACTGAAATCATTAAGCTATTCAAGACTCAAAATTTCTAAATTTTCTGACAGT 962
Qy 900 ATGATGTAATTAATGCTCATGATGATGATGATGATGATGATGATGATGATG 959
Db 963 ATGATGTAATTAATGCTCATGATGATGATGATGATGATGATGATGATGATG 1022
Qy 960 AAGATGAGCAATGATTAATTTTCACTTCAAAAGAGAGAGAGAGAGAGAGAGAG 1019
Db 1023 AAGATGAGCAATGATTAATTTTCACTTCAAAAGAGAGAGAGAGAGAGAGAGAG 1082
Qy 1020 AGTGAAGATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1079
Db 1083 AGTGAAGATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1142
Qy 1080 ACTTAATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1139
Db 1143 ACTTAATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1202
Qy 1140 ATGATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1199
Db 1203 ATGATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1262
Qy 1200 AGTGAATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1259
Db 1263 AGTGAATTAATTAATGCTGTAAGAAATCAATGAAATGATCTTTTGAAGATC 1322
Qy 1260 TTTTAAATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1319
Db 1323 TTTTAAATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1382
Qy 1320 TAAAAAATTTTGAAGATGATGATGATGATGATGATGATGATGATGATGATG 1346
Db 1383 TGAATGAG 1409

RESULT 511

US-10-097-065-17
; Sequence 17, Application US/10097065
; Publication No. US2003005236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US96/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,008
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,365
; PRIOR FILING DATE: 1997-12-19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 17
; LENGTH: 1432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-065-17
Query Match 98.5%; Score 1325.4; DB 15; Length 1432;
Best Local Similarity 99.5%; Pred. No. 7e-291;
Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
Qy 1 GAAAGAAATGTTGAGCTGCTCTTTTCTGATGATGATGATGATGATGATGATGAT 60
Db 63 GAAAGAAATGTTGAGCTGCTCTTTTCTGATGATGATGATGATGATGATGATGAT 122
Qy 61 CCAAGTCCAAATAATGCTTTTAAAGTGAAGCTTAAGTGAAGAGAGAGAGAGAT 120
Db 123 CCAAGTCCAAATAATGCTTTTAAAGTGAAGCTTAAGTGAAGAGAGAGAGAT 182
Qy 121 GCATATGCTGAGATACCAATGAAGATACCTCTTCAAGAGATGATGATGATGATGAT 180
Db 183 GCATATGCTGAGATACCAATGAAGATACCTCTTCAAGAGATGATGATGATGATGAT 242
Qy 181 AGAAAGTTCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 243 AGAAAGTTCCCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 302
Qy 241 CAGAGGATACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 303 CAGAGGATACATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
Qy 301 GTTGAAGTGAATCAGCCATTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 363 GTTGAAGTGAATCAGCCATTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAG 422

OY	840	CACACCTGAATTCATTAGCCCTTCAACGCCTCAAAATATCTCAAATAATTTTTCGAAGT	899
Db	851	CACACTGAAATCATTAGCTATCAACACTCAAAAATATCTCAAATAATTTTTCGAAGT	910
OY	900	ATTAGTGTTAAATGTGGTCATGTGGTAATTTGTAGTTATGTAAAGCATTTTAGAAAT	959
Db	911	ATTAGTGTTAAATGTGGTCATGTGGTAATTTGTAGTTATGTAAAGCATTTTAGAAAT	970
OY	960	AAGATCAGGCAATATGTAATATATTTTCA CACTTCAAGAAGCTTAGAGAAAAATTAATTTCC	1019
Db	971	AAGATCAGGCAATATGTAATATATTTTCA CACTTCAAGAAGCTTAGAGAAAAATTAATTTCC	1030
OY	1020	AGTGAGAAATCATATTAATATGTGTAGAAATTCATTGAAATNGATCTTTTTCAGATC	1079
Db	1031	AGTGAGAAATCATATTAATATGTGTAGAAATTCATTGAAATNGATCTTTTTCAGATC	1090
OY	1080	ACTTATATCACTCTGTAATATGACTAAGTAAACAAGAGAGAAATTAATTTGTAAATGG	1139
Db	1091	ACTTATATCACTCTGTAATATGACTAAGTAAACAAGAGAGAAATTAATTTGTAAATGG	1150
OY	1140	ATGATAAAAAATGNAATTTACTCATATPACAGGGTGAATTTTATCTGTATACACCAC	1199
Db	1151	ATGATAAAAAATGGAATTTACTCATATPACAGGGTGAATTTTATCTGTATACACCAC	1210
OY	1200	AGTTGATTATATATTTTTCTGAATATCACGCCCTATATAGACAAATTTATTTGTGACCAT	1259
Db	1211	AGTTGATTATATATTTTTCTGNAATATCACGCCCTATATATAGACAAATTTATTTGTGACCAT	1270
OY	1260	TTCTTCAATTTGTAAAGTCCCAATCTGTGCTAACTTAATTAAGTATATATCATCTTTT	1319
Db	1271	TTCTTCAATTTGTAAAGTCCCAATCTGTGCTAACTTAATTAAGTATATATCATCTCAAAA	1330
OY	1320	TAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1345
Db	1331	AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1356

RESULT 515
US-10-097-065-122
Sequence 122, Application US/10097065
Publication No. US20030055236A1
GENERAL INFORMATION:
APPLICANT: Moore, Paul A. et al.
TITLE OF INVENTION: 110 Human Secreted Proteins
FILE REFERENCE: P2021pi
CURRENT APPLICATION NUMBER: US/10/037, 065
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: PCT/US98/27059
PRIOR FILING DATE: 1998-12-17
PRIOR APPLICATION NUMBER: 60/070, 923
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 007
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 057
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 006
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 369
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068, 367
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068, 368
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068, 169
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 60/068, 053
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 064
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 054
PRIOR FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: 60/068, 008
PRIOR FILING DATE: 1997-12-18

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: PRIOR APPLICATION NUMBER: 60/068,365
: PRIOR FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 672
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 122
: LENGTH: 1356
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: SITE
: LOCATION: (1231)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-097-065-122

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Query Match	97.0%	Score 1305;	DB 15;	Length 1356;
Best Local Similarity	99.0%	Pred. No. 2.9e-286;		
Matches 1333; Conservative	0;	Mismatches 11;	Indels 2;	Gaps 2;

QY	1	GAAGAAATGTGTGGCTGCTCTTTTTCGTGTGACGTGCATTCAGCTGAACCTGTGCA	60
DB	12	GAAGAAATGTGTGGCTGCTCTTTTTCGTGTGACTGCCATTCAATGTGAACCTGTGCA	71
QY	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAAGACTTGTAGTACAGAACAGCTCTGGGAATATA	120
DB	72	CCAGGTGCAGAAAATGCTTTTAAAGTGAAGACTTGTAGTACAGAACAGCTCTGGGAATATA	131
QY	121	GCATATGCTGTGGGATPCCATAGAAATPACCTCTCAAGAGGATGTATGCTTCTCCAGT	180
DB	132	GCATATGCTGTGGGATPCCATAGAAATPACCTCTCAAGAGGATGTATGCTTCTCCAGT	191
QY	181	AGAAAAGTTCCTCCACAGAGAAAGCAACAGAAATTTCCCATGTCTACTTGTGCATATGAC	240
DB	192	AGAAAAGTTCCTCCACAGAGAAAGCAACAGAAATTTCCCATGTCTACTTGTGCATATGAC	251
QY	241	CAGAGGGTATCATTTCTGTGTGTGTGTGTTACAGACCTTGAAAAATACACCCCTTCTGT	300
DB	252	CAGA-GGTATCATTTCTGTGTGTGTGTGTTACAGACCTTGAAAAATACACCCCTTCTGT	310
QY	301	GTTGAGGTGCATCAGGCCATAGAAATGAAACAGAAACCGATACCAATATGCTTCTTCTA	360
DB	311	GTTGAGGTGCATCAGGCCATAGAAATGAAACAGAAACCGATACCAATATGCTTCTTCTA	370
QY	361	AATGACCAACCTCTGGAATTTTAAAAATCCCTTCACACTTGCACCAACCAATGACCA	420
DB	371	AATGACCAACCTCTGGAATTTTAAAAATCCCTTCACACTTGCACCAACCAATGACCA	430
QY	421	TCTGTGCCCATCTGGAATTTATATATTTGTGTGATATTTTGCAATCATATGTTCCATT	480
DB	431	TCTGTGCCCATCTGGAATTTATATATTTGTGTGATATTTTGCAATCATATGTTCCATT	490
QY	481	GCACATCATGATTTTATACAGGGATCTGGCAAGTAGAAGAAAAGAACAAAGAACCTCTGAA	540
DB	491	GCACATCATGATTTTATACAGGGATCTGGCAAGTAGAAGAAAAGAACAAAGAACCTCTGAA	550
QY	541	GTTGATGACGCTGGAAGATAGTGTGAAAACATGATCAATATGAAAAATGGCAATCCCTCT	600
DB	551	GTTGATGACGCTGGAAGATAGTGTGAAAACATGATCAATATGAAAAATGGCAATCCCTCT	610
QY	601	GATCCCTCTGACATGAAAGGG-GGGCATTTATATGATGCTTCTATGACAGAGATAGAGGG	659
DB	611	GATCCCTCTGACATGAAAGAGGGGCATTTATATATGATGCTTCTATGACAGAGATAGAGGG	670
QY	660	CTCACCCCTCTCTAAGAGGGCTGTGTCTGCTCTCTCAAGAAATTAACATTTGTCTTG	719
DB	671	CTCACCCCTCTCTAAGAGGGCTGTGTCTGCTCTCTCAAGAAATTAACATTTGTCTTG	730
QY	720	TGTATCTGCTGAGCATCTGAAATPCCAAAGACAGATCATATATTTGTTCACATCT	779
DB	731	TGTATCTGCTGAGCATCTGAAATPCCAAAGACAGATCATATATTTGTTCACATCT	790
QY	780	TCTTTTGTAAATATTTTGAATATGTCTGAAAGTGAAGAAAGCAATCAATTAATCCACCA	839
DB	791	TCTTTTGTAAATATTTTGAATATGTCTGAAAGTGAAGAAAGCAATCAATTAATCCACCA	850

Qy	840	CACCACTGAATATCATTAACCTATATCAAGCTCAAGCTCAAAATATATCTAAATATTTTCTGCAGCT	899
Db	851	CACCACTGAATATCATTAACCTATATCAAGCTCAAGCTCAAAATATATCTAAATATTTTCTGCAGCT	910
Qy	900	ATAGTGTATTAATGTGCTCATGTGGTATTTGTAGTATTTGATTTTAAAGATTTTAAAGAT	959
Db	911	ATAGTGTATTAATGTGCTCATGTGGTATTTGTAGTATTTGATTTTAAAGATTTTAAAGAT	970
Qy	960	AAGATCAGCATATGTATATATATTTTCAACCTTCAAAAGACTTAAGGAAAAATTAATTTTCC	1019
Db	971	AAGATCAGCATATGTATATATATTTTCAACCTTCAAAAGACTTAAGGAAAAATTAATTTTCC	1030
Qy	1020	AGTGGAGATACATTTATATATGTGTAGAAATCATTTGAAATTTGATCTTTTTCACATC	1079
Db	1031	AGTGGAGATACATTTATTAATGTGTAGAAATCATTTGAAATTTGATCTTTTTCACATC	1090
Qy	1080	ACTTATATACCTCTGTATATATGACTAAGTAACTAAAGGAGAGATTAATTTATTTAAATGG	1139
Db	1091	ACTTATATACCTCTGTATATATGACTAAGTAACTAAAGGAGAGATTAATTTATTTAAATGG	1150
Qy	1140	ATGCTATAAAAATGCAATTAATCTCATATACAGGGTGAATTTTATCTGTATACACCAAC	1199
Db	1151	ATGCTATAAAAATTTGAATTAATCTCATATACAGGGTGGATTTTATCTGTATACACCAAC	1210
Qy	1200	AGTTGATTAATATATTTTCTGATATATCAGCCCTTAATAGACAATTTCTATTTTGACCAT	1259
Db	1211	AGTTGATTAATATATTTTCTGATATATCAGCCCTTAATAGACAATTTCTATTTTGACCAT	1270
Qy	1260	TTCTACAAATTTGTAAATGCTCAATCTGTGCTAACCTTAATAGTAATATATCATCTCTTT	1319
Db	1271	TTCTACAAATTTGTAAATGCTCAATCTGTGCTAACCTTAATAGTAATATATCATCAAAAA	1330
Qy	1320	TAATAAAAAAAAAAAAAAAAAAAAAA	1345
Db	1331	AAAAAAAAAAAAAAAAAAAAAAAAAAAA	1356
RESULT 516			
US-10-133-013-205			
Sequence 205, Application US/10133013			
Publication No. US20030166903A1			
GENERAL INFORMATION:			
APPLICANT: Astromoff, Anna			
APPLICANT: Bandman, Olga			
APPLICANT: Cocks, Benjamin G.			
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE			
FILE REFERENCE: PA-0049 US			
CURRENT APPLICATION NUMBER: US/10/133.013			
CURRENT FILING DATE: 2002-04-25			
PRIOR APPLICATION NUMBER: 60/287,067			
PRIOR FILING DATE: 2001-04-27			
NUMBER OF SEQ ID NOS: 271			
SOFTWARE: PERL Program			
SEQ ID NO 205			
LENGTH: 1312			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURES:			
NAME/KEY: misc_feature			
OTHER INFORMATION: Incyte ID No. US20030166903A1 2580580CB1			
US-10-133-013-205			

Query Match	96.4%	Score 1297	DB 15	Length 1112
Best Local Similarity	99.9%	Pred. No. 1.9e-284		
Matches 1308	Conservative 0	Mismatches 0	Indels 1	Gaps 1
Oy	1	GAAGAAATGTTGGAGCTCTTTTTCCTGGAGCTCCATTCATGCTGAACCTCTGCA	60	
Db	3	GAAGAAATGTTGGAGCTCTTTTTCCTGGAGCTCCATTCATGCTGAACCTCTGCA	62	
Oy	61	CCAGGTGAGAAATGCTTTTAAGTGAAGCTTAAGTGAAGAGCTCTGGAGATAA	120	

D	63	CCAGGTGCAGAAAATGCTTTAAAGTGAAGCTTAGTATCAGAAACGCTGTGGAGATATA	122
Q	121	GCATATGCTGGGATACCAATGAAAGATACCTCTTCAAGCGATGTAAGCTTCTCAATG	180
D	123	GCATATGCTGGGATACCAATGAAAGATACCTCTTCAAGCGATGTAAGCTTCTCAATG	182
Q	181	AGAAAAGTTCGCCAACAGAGAGCAACGAATTTCCCAATGTCATCTTTGCAATGTAAC	240
D	183	AGAAAAGTTCGCCAACAGAGAGCAACGAATTTCCCAATGTCATCTTTGCAATGTAAC	242
Q	241	CAGAGGGATATCTGTGTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCT	300
D	243	CAGAGGGATATCTGTGTTGTGGTTACAGACCCTTCAAAAAATCACACCCTTCTGCT	302
Q	301	GTTGAGTGCAATCAGCCATTAGATGAAACAAGAACCGATCAACATGCTTCTTCTA	360
D	303	GTTGAGTGCAATCAGCCATTAGATGAAACAAGAACCGATCAACATGCTTCTTCTA	362
Q	361	AATGACCAACTCTGGAATTTTAAAAATCCCTTCCACCTTGACCCACCAATGACCA	420
D	363	AATGACCAACTCTGGAATTTTAAAAATCCCTTCCACCTTGACCCACCAATGACCA	422
Q	421	TCTGAGCCATCTGATATATATATTTGGTGTGATATTTTGCATCATCATATGTTGCAAT	480
D	423	TCTGAGCCATCTGATATATATATTTGGTGTGATATTTTGCATCATCATATGTTGCAAT	482
Q	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAGAGAAAGAACAAAGAACATCTGAA	540
D	483	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAGAGAAAGAACAAAGAACATCTGAA	542
Q	541	GTCGATGACGCTGAAGATTAAGTGTGAAAACTGATCAGATTGAAAAATGCAATCCCTCT	600
D	543	GTCGATGACGCTGAAGATTAAGTGTGAAAACTGATCAGATTGAAAAATGCAATCCCTCT	602
Q	601	GATCCCTCGACATGAAGGGG-GGGCATATTAATGATGCTTCATGACAGAGATGAGAG	659
D	603	GATCCCTCGACATGAAGGGGCAATATTAATGATGCTTCATGACAGAGATGAGAG	662
Q	660	CTCACCCCTCTCTGAAGGGCTGTGTCTCTGCTTCTCAAGAAATTAACATTTGTCTG	719
D	663	CTCACCCCTCTCTGAAGGGCTGTGTCTCTGCTTCTCAAGAAATTAACATTTGTCTG	722
Q	720	TGTGATGCTGAGCATCTGAAATACCAAGCGCATATATTTTGTTCACACATCT	779
D	723	TGTGATGCTGAGCATCTGAAATACCAAGCGCATATATTTTGTTCACACATCT	782
Q	780	TCTTTGTAAATAATTTTGAATGTGCTTGAAGGAAGCAATCAATTAACCAACA	839
D	783	TCTTTGTAAATAATTTTGAATGTGCTTGAAGGAAGCAATCAATTAACCAACA	842
Q	840	CACCACTGAATCATTAAGCTATTACACATCAAAATATCTTAATAATTTTCTGACAGT	899
D	843	CACCACTGAATCATTAAGCTATTACACATCAAAATATCTTAATAATTTTCTGACAGT	902
Q	900	ATAGTGTAAATATGTGTCATGTGTAATTTGTAGTATTTGAATTTTAAGCATTTTGAAT	959
D	903	ATAGTGTAAATATGTGTCATGTGTAATTTGTAGTATTTGAATTTTGAAT	962
Q	960	AAGATCAGGCATATGTAATTTTTCACATTCACAAAGCCTAAGGAAAAATTAATTTTCC	1019
D	963	AAGATCAGGCATATGTAATTTTTCACATTCACAAAGCCTAAGGAAAAATTAATTTTCC	1022
Q	1020	AGTGAAGAAATCATATATATATGTGTGAATCATTTGAATAATGATCTTTTGAACATC	1079
D	1023	AGTGAAGAAATCATATATATATGTGTGAATCATTTGAATAATGATCTTTTGAACATC	1082
Q	1080	ACTATATCACTCTGATATATGACTAAGTAAACAAAGTGAGAGTAATTAATTGAATGG	1139
D	1083	ACTATATCACTCTGATATATGACTAAGTAAACAAAGTGAGAGTAATTAATTGAATGG	1142
Q	1140	ATGATATAAAAATGAATTAATCAATATACAGGTGGAATTTTATCTGTATCACACCAAC	1199
D	1143	ATGATATAAAAATGAATTAATCAATATACAGGTGGAATTTTATCTGTATCACACCAAC	1202

Oy 1200 AGTGATTATATATTTTCTGAATATCAGCCCTAATAGACAATTCATTGTGACCAT 1259
 |||||
 Db 1203 AGTGATTATATATTTTCTGAATATCAGCCCTAATAGACAATTCATTGTGACCAT 1262
 |||||
 Oy 1260 TTCTACAATTTGTAAAGTCCAATCTGTGCTAATTATTAAGTAAATA 1308
 |||||
 Db 1263 TTCTACAATTTGTAAAGTCCAATCTGTGCTAATTATTAAGTAAATA 1311
 |||||

Search completed: June 6, 2004, 16:41:21
 Job time : 772.663 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 07:26:44 ; Search time 258.223 Seconds

(without alignments)
10496.171 Million cell updates/sec

Title: US-09-989-724-386_COPY_7_644

Perfect score: 638
Sequence: 1 atgttggtgctgctctttt.....atataatgagctctcatg 638

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 234

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 80%

Maximum Match 100%

Listing first 65000 summaries

Database :

1: N_Geneseq_29Jan04:.*
2: geneseqn1980s:.*
3: geneseqn1990s:.*
4: geneseqn2000s:.*
5: geneseqn2001as:.*
6: geneseqn2002s:.*
7: geneseqn2003as:.*
8: geneseqn2003bs:.*
9: geneseqn2003cs:.*
10: geneseqn2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	638	100.0	1346	AAZ65097	Membrane-
2	638	100.0	1346	AAZ65097	Membrane-
3	638	100.0	1346	AAZ65097	Membrane-
4	638	100.0	1346	AAZ65097	Membrane-
5	638	100.0	1346	AAZ65097	Membrane-
6	638	100.0	1346	AAZ65097	Membrane-
7	638	100.0	1346	AAZ65097	Membrane-
8	638	100.0	1346	AAZ65097	Membrane-
9	638	100.0	1346	AAZ65097	Membrane-
10	638	100.0	1346	AAZ65097	Membrane-
11	638	100.0	1346	AAZ65097	Membrane-
12	638	100.0	1346	AAZ65097	Membrane-
13	638	100.0	1346	AAZ65097	Membrane-
14	638	100.0	1346	AAZ65097	Membrane-
15	638	100.0	1346	AAZ65097	Membrane-
16	638	100.0	1346	AAZ65097	Membrane-
17	638	100.0	1346	AAZ65097	Membrane-
18	638	100.0	1346	AAZ65097	Membrane-
19	638	100.0	1346	AAZ65097	Membrane-
20	638	100.0	1346	AAZ65097	Membrane-
21	638	100.0	1346	AAZ65097	Membrane-
22	638	100.0	1346	AAZ65097	Membrane-
23	638	100.0	1346	AAZ65097	Membrane-

24	638	100.0	1346	7	ABX17158	Abx17158 Human PRO
25	638	100.0	1346	8	ACA68013	ACA68013 Human PRO
26	638	100.0	1346	8	ACA88462	ACA88462 Human PRO
27	638	100.0	1346	8	ACD81969	ACD81969 Human PRO
28	638	100.0	1346	8	ADA66000	ADA66000 Human PRO
29	638	100.0	1346	8	ADA76431	ADA76431 Human PRO
30	638	100.0	1346	8	ADA19081	ADA19081 Human PRO
31	638	100.0	1346	8	ADA61704	ADA61704 Human PRO
32	638	100.0	1346	8	ADB19489	ADB19489 Human PRO
33	638	100.0	1346	8	ADB28030	ADB28030 Human PRO
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37	638	100.0	1346	8	ADA47859	ADA47859 Human PRO
38	638	100.0	1346	8	ADA21583	ADA21583 Human PRO
39	638	100.0	1346	8	ADA10370	ADA10370 Human PRO
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42	638	100.0	1346	8	ADA85957	ADA85957 Human PRO
43	638	100.0	1346	8	ADA17914	ADA17914 Human PRO
44	638	100.0	1346	8	ADA97169	ADA97169 Human PRO
45	638	100.0	1346	8	ADA79473	ADA79473 Human PRO
46	638	100.0	1346	8	ADA87612	ADA87612 Human PRO
47	638	100.0	1346	8	ADB16814	ADB16814 Human PRO
48	638	100.0	1346	8	ADA28022	ADA28022 Human PRO
49	638	100.0	1346	8	ADA91906	ADA91906 Human PRO
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51	638	100.0	1346	8	ADB18930	ADB18930 Human PRO
52	638	100.0	1346	8	ADA94145	ADA94145 Human PRO
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54	638	100.0	1346	8	ADB13353	ADB13353 Human PRO
55	638	100.0	1346	8	ACD98664	ACD98664 Human PRO
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57	638	100.0	1346	8	ADA74607	ADA74607 Human PRO
58	638	100.0	1346	8	ADB24840	ADB24840 Human PRO
59	638	100.0	1346	8	ADA82364	ADA82364 Human PRO
60	638	100.0	1346	8	ADA75327	ADA75327 Human PRO
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62	638	100.0	1346	8	ADA84853	ADA84853 Human PRO
63	638	100.0	1346	8	ADB30109	ADB30109 Human PRO
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87	638	100.0	1346	8	ACH65530	ACH65530 Human PRO
88	638	100.0	1346	8	ADA77086	ADA77086 Human PRO
89	638	100.0	1346	8	ADA22509	ADA22509 Human PRO
90	638	100.0	1346	8	ADA88716	ADA88716 Human PRO
91	638	100.0	1346	8	ADA97721	ADA97721 Human PRO
92	638	100.0	1346	8	ADA27478	ADA27478 Human PRO
93	638	100.0	1346	8	ADB22411	ADB22411 Human PRO
94	638	100.0	1346	8	ACD39520	ACD39520 Human PRO
95	638	100.0	1346	8	ADA06675	ADA06675 Human PRO
96	638	100.0	1346	8	ADA39368	ADA39368 Human PRO

97	638	100.0	1346	8	ADb67102	Human PRO	170	638	100.0	1346	9	ADb26909	Novel hum	ADb26909
98	638	100.0	1346	8	ADb22963	Human PRO	171	638	100.0	1346	9	ADb32422	Novel hum	ADb32422
99	638	100.0	1346	8	ADb33736	Human PRO	172	638	100.0	1346	9	ADb22354	CDNA enco	ADb22354
100	638	100.0	1346	8	ADb92458	Novel hum	173	638	100.0	1346	9	ADb79578	CDNA enco	ADb79578
101	638	100.0	1346	8	ADb15521	Human PRO	174	638	100.0	1346	9	ADb42114	Human PRO	ADb42114
102	638	100.0	1346	8	ADb38773	Novel hum	175	638	100.0	1346	9	ADb17931	Human PRO	ADb17931
103	638	100.0	1346	8	ADb96394	Human PRO	176	638	100.0	1346	9	ADb92063	Human PRO	ADb92063
104	638	100.0	1346	8	ADb38221	Novel hum	177	638	100.0	1346	9	ADb33526	Novel hum	ADb33526
105	638	100.0	1346	8	ADb66693	Novel hum	178	638	100.0	1346	9	ADb34078	Novel hum	ADb34078
106	638	100.0	1346	9	ADb89773	Human PRO	179	638	100.0	1346	9	ADb80130	CDNA enco	ADb80130
107	638	100.0	1346	9	ADb90505	Human PRO	180	638	100.0	1346	9	ADb93167	Human PRO	ADb93167
108	638	100.0	1346	9	ADb39606	Novel hum	181	638	100.0	1346	9	ADb19587	Human PRO	ADb19587
109	638	100.0	1346	9	ADb47229	Novel hum	182	638	100.0	1346	9	ADb19035	Human PRO	ADb19035
110	638	100.0	1346	9	ADb86836	Human PRO	183	638	100.0	1346	9	ADb34321	Human PRO	ADb34321
111	638	100.0	1346	9	ADb77441	Novel hum	184	638	100.0	1346	9	ADb96020	Human PRO	ADb96020
112	638	100.0	1346	9	ADb34598	Human PRO	185	638	100.0	1346	9	ADb22906	CDNA enco	ADb22906
113	638	100.0	1346	9	ADb35702	Human PRO	186	638	100.0	1346	9	ADb79024	CDNA enco	ADb79024
114	638	100.0	1346	9	ADb34046	Human PRO	187	638	100.0	1346	9	ADb26376	Novel hum	ADb26376
115	638	100.0	1346	9	ADb35150	Human PRO	188	638	100.0	1346	9	ADb32974	Novel hum	ADb32974
116	638	100.0	1346	9	ADb36254	Human PRO	189	638	100.0	1346	9	ADb42666	Human PRO	ADb42666
117	638	100.0	1346	9	ADb46649	Novel hum	190	638	100.0	1346	9	ADb80682	CDNA enco	ADb80682
118	638	100.0	1346	9	ADb57866	Human PRO	191	638	100.0	1346	9	ADb89710	Human PRO	ADb89710
119	638	100.0	1346	9	ADb55230	Human PRO	192	638	100.0	1346	9	ADb40994	Human PRO	ADb40994
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121	638	100.0	1346	9	ADb56519	Human PRO	194	638	100.0	1346	10	ADb81218	Novel hum	ADb81218
122	638	100.0	1346	9	ADb07574	Human PRO	195	638	100.0	1346	10	ADb76666	Human PRO	ADb76666
123	638	100.0	1346	9	ADb11564	Human PRO	196	638	100.0	1346	10	ADb88030	Human PRO	ADb88030
124	638	100.0	1346	9	ADb05052	Novel hum	197	638	100.0	1346	10	ADb86434	Human PRO	ADb86434
125	638	100.0	1346	9	ADb072069	Novel hum	198	638	100.0	1346	10	ADb75882	Human PRO	ADb75882
126	638	100.0	1346	9	ADb60048	Novel hum	199	638	100.0	1346	10	ADb23458	CDNA enco	ADb23458
127	638	100.0	1346	9	ADb35055	Novel hum	200	638	100.0	1346	10	ADb24010	CDNA enco	ADb24010
128	638	100.0	1346	9	ADb57409	Novel hum	201	638	100.0	1346	10	ADb24653	CDNA enco	ADb24653
129	638	100.0	1346	9	ADb60600	Novel hum	202	638	100.0	1346	10	ADb87478	Human PRO	ADb87478
130	638	100.0	1346	9	ADb51075	Novel hum	203	638	100.0	1346	10	ADb89344	Human PRO	ADb89344
131	638	100.0	1346	9	ADb56602	Human PRO	204	638	100.0	1346	10	ADb18483	Human PRO	ADb18483
132	638	100.0	1346	9	ADb34700	Novel hum	205	638	100.0	1346	10	ADb88792	Human PRO	ADb88792
133	638	100.0	1346	9	ADb53661	Novel hum	206	638	100.0	1346	10	ADb94460	Human PRO	ADb94460
134	638	100.0	1346	9	ADb59184	Novel hum	207	638	100.0	1346	7	ADb94470	Human PRO	ADb94470
135	638	100.0	1346	9	ADb50682	Novel hum	208	638	100.0	1346	7	ADb56090	Gene enco	ADb56090
136	638	100.0	1346	9	ADb58632	Novel hum	209	638	100.0	1346	8	ADb39900	Human PRO	ADb39900
137	638	100.0	1346	9	ADb14686	Novel hum	210	638	100.0	1346	8	ADb11489	Human PRO	ADb11489
138	638	100.0	1346	9	ADb08218	Novel hum	211	638	100.0	1346	9	ADb37613	Human PRO	ADb37613
139	638	100.0	1346	9	ADb03306	Novel hum	212	638	100.0	1346	9	ADb25261	Human PRO	ADb25261
140	638	100.0	1346	9	ADb09298	Novel hum	213	638	100.0	1346	9	ADb11650	Human PRO	ADb11650
141	638	100.0	1346	9	ADb82043	Human PRO	214	638	100.0	1346	7	ADb78127	Human PRO	ADb78127
142	638	100.0	1346	9	ADb69717	CDNA enco	215	638	100.0	1346	2	ADb40540	Homo sapi	ADb40540
143	638	100.0	1346	9	ADb48606	Human PRO	216	638	100.0	1346	2	ADb19983	Human PRO	ADb19983
144	638	100.0	1346	9	ADb10135	Human PRO	217	638	100.0	1346	2	ADb39430	Human PRO	ADb39430
145	638	100.0	1346	9	ADb07685	Novel hum	218	638	100.0	1346	2	ADb41369	Extended	ADb41369
146	638	100.0	1346	9	ADb04710	Novel hum	219	638	100.0	1346	2	ADb97564	Extended	ADb97564
147	638	100.0	1346	9	ADb042576	Human PRO	220	638	100.0	1346	2	ADb26772	Secreted	ADb26772
148	638	100.0	1346	9	ADb08066	Novel hum	221	638	100.0	1346	2	ADb51777	Human PRO	ADb51777
149	638	100.0	1346	9	ADb11173	Human PRO	222	638	100.0	1346	2	ADb51449	Human PRO	ADb51449
150	638	100.0	1346	9	ADb48054	Human PRO	223	638	100.0	1346	2	ADb40428	Extended	ADb40428
151	638	100.0	1346	9	ADb08756	Novel hum	224	638	100.0	1346	3	ADb42251	Human PRO	ADb42251
152	638	100.0	1346	9	ADb80114	Novel hum	225	638	100.0	1346	2	ADbC0012	Human PRO	ADbC0012
153	638	100.0	1346	9	ADb07005	Novel hum	226	638	100.0	1346	2	ADb88191	Human PRO	ADb88191
154	638	100.0	1346	9	ADb09583	Human PRO	227	638	100.0	1346	2	ADb31063	Human PRO	ADb31063
155	638	100.0	1346	9	ADb3252	Human PRO	228	638	100.0	1346	4	ADb98224	Human EST	ADb98224
156	638	100.0	1346	9	ADb41296	Novel hum	229	638	100.0	1346	2	ADb97957	Human PRO	ADb97957
157	638	100.0	1346	9	ADb52435	CDNA enco	230	638	100.0	1346	2	ADb55445	Gene enco	ADb55445
158	638	100.0	1346	9	ADb53175	CDNA enco	231	638	100.0	1346	7	ADb40381	Human PRO	ADb40381
159	638	100.0	1346	9	ADb53727	Novel hum	232	638	100.0	1346	8	ADb11594	Human PRO	ADb11594
160	638	100.0	1346	9	ADb55359	Human PRO	233	638	100.0	1346	9	ADb37752	Human PRO	ADb37752
161	638	100.0	1346	9	ADb56317	Human PRO	234	638	100.0	1346	9	ADb37752	Human PRO	ADb37752
162	638	100.0	1346	9	ADb51883	CDNA enco								
163	638	100.0	1346	9	ADb02682	Human PRO								
164	638	100.0	1346	9	ADb02116	Human PRO								
165	638	100.0	1346	9	ADb54298	Novel hum								
166	638	100.0	1346	9	ADb54755	Human PRO								
167	638	100.0	1346	9	ADb92615	Human PRO								
168	638	100.0	1346	9	ADb91511	Human PRO								
169	638	100.0	1346	9	ADb04125	Human PRO								

ALIGNMENTS

RESULT 1
AA265097
ID AA265097 standard, CDNA; 1346 bp.

stimulating release of TNF-alpha from human blood.

Claim 2; SEQ ID NO 481; 638bp; English.

The invention relates to isolated human PRO polypeptides (secreted and transmembrane polypeptides) and the polynucleotides encoding them. The invention also relates to an antibody which specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, a method for stimulating the proliferation or differentiation of chondrocyte cells and a method for detecting the presence of a tumour in a mammal (e.g. adrenal, lung, colon, breast, prostate, rectal, kidney, cervical and liver tumours). The polynucleotides are useful in molecular biology, including uses as hybridisation probes, in chromosome and gene mapping, in generating antisense RNA and DNA and in gene therapy. The polynucleotides may also be used in preparing PRO polypeptides by recombinant techniques and in generating either transgenic animals or knock-out animals which are useful in the development and screening of therapeutically useful reagents. The PRO polypeptides or antibodies are used in preparing a medicament for treating a condition responsive to the polypeptides or antibodies, such as tumours, for stimulating and inhibiting proliferation of human microvascular endothelial cells, for modulating the uptake of glucose or FFA by skeletal muscle cells or adipocyte cells, for stimulating differentiation of adipocyte cells, for stimulating proliferation of or gene expression in pericyte cells, for stimulating the proliferation of inner ear utricular supporting cells or T-lymphocyte cells, for inducing endothelial cell tube formation and for treating various bone and/or cartilage disorders such as sports injuries and arthritis. PRO polypeptides which stimulate the release of proteoglycans from cartilage are useful for treating sports-related joint problems, articular cartilage defects, osteoarthritis and rheumatoid arthritis. PRO polypeptides are also useful for treating various mammalian haemoglobin-associated disorders such as various thalassemias and conditions which may benefit from enhanced local immune system cell infiltration. This sequence represents a human PRO polynucleotide of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 1346 BP; 457 A; 245 C; 237 G; 407 T; 0 U; 0 Other;

Query Match 100.0%; Score 638; DB 10; Length 1346;

Best Local Similarity 100.0%; Pred. No. 1.1e-184;

Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AAGTGTGGCTGCTCTTTTTCGAGACCTGACCTGAGTCTGCAACAGGT 60
7 ATGTTGTGGCTCTCTTTTTCGAGACCTGACCTGAGTCTGCAACAGGT 66
61 GCAGAAATGCTTTTAAAGTGAAGTCTGATCAGAAAGCTCTGGAGATTAAGCATAT 120
67 GCAGAAATGCTTTTAAAGTGAAGTCTGATCAGAAAGCTCTGGAGATTAAGCATAT 126
121 GCTTGGATACCAATGAAGATACCTTTCAAAAGCATGGTAGCTTTTCATGAGAAA 180
127 GCTTGGATACCAATGAAGATACCTTTCAAAAGCATGGTAGCTTTTCATGAGAAA 186
181 GTTCCACAGAGAGCAACAGAAATTTCCATGCTCTTGAATGTAACCCAGAG 240
187 GTTCCACAGAGAGCAACAGAAATTTCCATGCTCTTGAATGTAACCCAGAG 246
241 GATCATCTGCTGTTGTGTTACAGACCTTCAAAAATACACCCCTCTGCTGTGAG 300
247 GATCATCTGCTGTTGTGTTACAGACCTTCAAAAATACACCCCTCTGCTGTGAG 306
301 GTGCAATCAGCCATTAAGATGAAGAAACCGATCAACATGCTCTTCTTAATGAC 360
307 GTGCAATCAGCCATTAAGATGAAGAAACCGATCAACATGCTCTTCTTAATGAC 366
361 CAAACCTGGAAATTTTAAATATCCCTTCACACTGACCAACCCATGACCATCTG 420
367 CAAACCTGGAAATTTTAAATATCCCTTCACACTGACCAACCCATGACCATCTG 426
421 CCAATCTGGATTAATATTTGGTGTATATTTGATCATCATGATGTAATGACATA 480

|||||
427 CCAATCTGGATTAATATTTGGTGTATATTTGATCATCATGATGTAATGACATA 486
Qy 481 CTGATTTTACAGGAGATCTGCAACCTAGAAAGAAACAAAGACCATCTGAAGTGAAT 540
Db 487 CTGATTTTACAGGAGATCTGCAACCTAGAAAGAAACAAAGACCATCTGAAGTGAAT 546
Qy 541 GACGCTGAAGATTAAGTGTGAAAACATGATCATTGAAGAAATGGCATCCCTCTGATCCC 600
Db 547 GACGCTGAAGATTAAGTGTGAAAACATGATCATTGAAGAAATGGCATCCCTCTGATCCC 606
Qy 601 CTGAGATGAAAGGGGGCATTTTAATGATGCTTCAATG 638
Db 607 CTGAGATGAAAGGGGGCATTTTAATGATGCTTCAATG 644

RESULT 206

AAFP94460
ID AAFP94460 standard; cDNA; 666 BP.

AAFP94460;

04-JUN-2001 (first entry)

Human hydrophobic domain containing protein clone HP10720 cDNA #74.

Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective; antianemic; vulnary; antileuk; osteopathic; anti-inflammatory; cytostatic; gene therapy; autoimmune disorder; multiple sclerosis; HIV infection; anemia; burn; ulcer; osteoporosis; tumour; wound healing; inflammatory bowel disease; nutritional supplement; appetite; vaccine; behavioral characteristic; immune response; ss.

Homo sapiens.

MO200112660-A2.

22-FEB-2001.

10-AUG-2000; 2000MO-JP005356.

17-AUG-1999; 99JP-00230344.
07-SBP-1999; 99JP-00252551.
PR 01-OCT-1999; 99JP-00281132.
PR 22-OCT-1999; 99JP-00301624.
PR 04-NOV-1999; 99JP-00313877.

(SAGA) SAGAMI CHEM RES CENT.
(PROT-) PROTEGENE INC.

Kato S, Kilmura T;

WPI; 2001-160059/16.

P-PDB; AAB88580.

Human proteins with hydrophobic domains and the DNAs which encode them are useful for treating autoimmune disorders, burns and tumors and for screening novel pharmaceuticals.

Claim 3; Page 368; 518bp; English.

AAFP94417 to AAFP94516 encode the human proteins given in AAB88557 to AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant, anti-HIV, neuroprotective, antianemic, vulnary, antileuk, osteopathic, anti-inflammatory and cyrostatic activities, and can be used in gene therapy. (I) can be used as pharmaceuticals and as antigens to prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes for genetic diagnosis and gene sources for gene therapy or for producing (I) in large quantities. Cells containing (II) are used for the detection of ligands or receptors corresponding to membrane or secretory proteins and to screen small molecule novel pharmaceuticals. Antibodies directed to (I) can be used for the detection, quantification and purification of (I). Activities of (I) may include cytokine and cell

CC proliferation/differentiation function, immune stimulating or suppressing
 CC activity, haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory
 CC activity (I) and (II) can be used to treat autoimmune disorders e.g.
 CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
 CC inflammatory bowel disease and tumours. (I) and (II) can also be used for
 CC wound healing, as nutritional sources or supplements e.g. as amino acid,
 CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
 CC processing and utilisation of dietary fat, protein, carbohydrate,
 CC vitamins and minerals, to effect behavioural characteristics, to affect
 CC appetite, and can act as antigens in vaccines to raise an immune response
 CC to the protein or another material cross-reactive with the protein
 CC
 XX
 SQ Sequence 666 BP; 203 A; 148 C; 136 G; 179 T; 0 U; 0 Other;

Query Match 98.3%; Score 627; DB 4; Length 666;
 Best Local Similarity 99.8%; Pred. No. 1.9e-181;
 Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTGCGCGCTCTTTTCTGTGACCTGCACTGCAATGCTGAAGTCTGTCAACAGGT 60
 DB 1 ATGTGCGCGCTCTTTTCTGTGACCTGCACTGCAATGCTGAAGTCTGTCAACAGGT 60
 QY 61 GCAGAAATGCTTTTAAAGTGAAGCTTATGATCAGAAACAGCTCTGGAGATTAAGCATAT 120
 DB 61 GCAGAAATGCTTTTAAAGTGAAGCTTATGATCAGAAACAGCTCTGGAGATTAAGCATAT 120
 QY 121 GCGTGGATACCAATGAAATACCTCTTCAACAGATGATGATTTCTCCATAGAGAAA 180
 DB 121 GCGTGGATACCAATGAAATACCTCTTCAACAGATGATGATTTCTCCATAGAGAAA 180
 QY 181 GTTCCCAAG 240
 DB 181 GTTCCCAAG 240
 QY 241 GATTCATCTGTTTGTGTGTTACAGACCTTCAAAAATATCAACCTCTGCTGTGAG 300
 DB 241 GATTCATCTGTTTGTGTGTTACAGACCTTCAAAAATATCAACCTCTGCTGTGAG 300
 QY 301 GTGCAATCAGCCATTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB 301 GTGCAATCAGCCATTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 QY 361 CAAACTGTGAATTTTAAAAATCCCTTCCACACTTGGACCAACCATGAGTGTG 420
 DB 361 CAAACTGTGAATTTTAAAAATCCCTTCCACACTTGGACCAACCATGAGTGTG 420
 QY 421 CCATCTGATATTTATATTTGTGTGATATTTTGCATCATAGTTCATATTCAGTCA 480
 DB 421 CCATCTGATATTTATATTTGTGTGATATTTTGCATCATAGTTCATATTCAGTCA 480
 QY 481 CTGATTTTATCAGGATCTGGCAAGTGAAGAAAGAAAGAAAGCAATCTGAAGTGAAT 540
 DB 481 CTGATTTTATCAGGATCTGGCAAGTGAAGAAAGAAAGAAAGCAATCTGAAGTGAAT 540
 QY 541 GAGCGTAAGATTAAGTGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
 DB 541 GAGCGTAAGATTAAGTGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 600
 QY 601 CTGACATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 638
 DB 601 CTGACATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 638

RESULT 207
 AAF94470
 ID AAF94470 standard; cDNA; 1347 BP.

XX AAF94470;
 AC
 XX
 DT 04-JUN-2001 (first entry)
 XX

DE Human hydrophobic domain containing protein clone HP10720 cDNA #84.
 XX Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
 XX anti-anaemic; vulnery; antiulcer; osteopathic; anti-inflammatory;
 XX cyrostatic; gene therapy; autoimmune disorder; multiple sclerosis;
 XX HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
 XX inflammatory bowel disease; nutritional supplement; appetite; vaccine;
 XX behavioural characteristic; immune response; ss.

OS Homo sapiens.

PM MO200112660-42.

PD 22-FEB-2001.

PF 10-AUG-2000; 2000WO-JP005356.

PR 17-AUG-1999; 99JP-00230344.

PR 07-SEP-1999; 99JP-00252531.

PR 01-OCT-1999; 99JP-00281132.

PR 22-OCT-1999; 99JP-00301624.

PR 04-NOV-1999; 99JP-00313877.

PA (SAGA) SAGAMI CHEM RES CENT.

PI (PROT-) PROTEGENE INC.

PI Kato S, Kimura T;

XX WPI: 2001-160059/16.

DR P-PSDB; AAB88580.

PT Human proteins with hydrophobic domains and the DNAs which encode them

PT are useful for treating autoimmune disorders, burns and tumors and for

PT screening novel pharmaceuticals.

XX Claim 4; Page 384-386; 518pp; English.

XX AAF94417 to AAF94516 encode the human proteins given in AAB88557 to

XX AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,

XX anti-HIV, neuroprotective, anti-anaemic, vulnery, antiulcer,

XX osteopathic, anti-inflammatory and cyrostatic activities, and can be used

XX in gene therapy. (I) can be used as pharmaceuticals and as antigens to

XX prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes

XX for genetic diagnosis and gene sources for gene therapy or for producing

XX (I) in large quantities. Cells containing (II) are used for the detection

XX of ligands or receptors corresponding to membrane or secretory proteins

XX and to screen small molecule novel pharmaceuticals. Antibodies directed

XX to (I) can be used for the detection, quantification and purification of

XX (I). Activities of (I) may include cytokine and cell

XX proliferation/differentiation function, immune stimulating or suppressing

XX activity, haematopoiesis regulating activity, tissue growth activity,
 CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, receptor/ligand activity and anti-inflammatory
 CC activity. (I) and (II) can be used to treat autoimmune disorders e.g.
 CC multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
 CC inflammatory bowel disease and tumours. (I) and (II) can also be used for
 CC wound healing, as nutritional sources or supplements e.g. as amino acid,
 CC carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
 CC processing and utilisation of dietary fat, protein, carbohydrate, vitamin
 CC and minerals, to effect behavioural characteristics, to affect
 CC appetite, and can act as antigens in vaccines to raise an immune response
 CC to the protein or another material cross-reactive with the protein
 CC
 XX
 SQ Sequence 1347 BP; 434 A; 252 C; 243 G; 418 T; 0 U; 0 Other;

Query Match 98.3%; Score 627; DB 4; Length 1347;
 Best Local Similarity 99.8%; Pred. No. 2.6e-181;
 Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTGCGCGCTCTTTTCTGTGACCTGCACTGCAATGCTGAAGTCTGTCAACAGGT 60
 DB 26 ATGTGCGCGCTCTTTTCTGTGACCTGCACTGCAATGCTGAAGTCTGTCAACAGGT 85

QY 61 GCGAGAAAATGCTTTTAAAGTGAAGCTTACCTAGTACAGAAAGCTTGGAGATAAGCATAT 120
 DB 86 GCGAGAAAATGCTTTTAAAGTGAAGCTTACCTAGTACAGAAAGCTTGGAGATAAGCATAT 145
 QY 121 GCGTGGAGATACCAATGAATATCTCTTCAAGGAGATGATCTTCTCCATGAGAAA 180
 DB 146 GCGTGGAGATACCAATGAATATCTCTTCAAGGAGATGATCTTCTCCATGAGAAA 205
 QY 181 GTTCCCAAGAGAAAGCAAGAAATTTCCCATGCTCTTCTTGGCAATGTAAACCAAGG 240
 DB 206 GTTCCCAAGAGAAAGCAAGAAATTTCCCATGCTCTTCTTGGCAATGTAAACCAAGG 265
 QY 241 GTATCATTTCTGTTGTGTGTACAGACCTTCAAAAATATACACCTTCTCTGTTGAG 300
 DB 266 GTATCATTTCTGTTGTGTGTGTACAGACCTTCAAAAATATACACCTTCTCTGTTGAG 325
 QY 301 GTGCAATCAGCATTAAGATGAAGCAAGAAACCGGATCAAGATCCTTCTTAAATGAC 360
 DB 326 GTGCAATCAGCATTAAGATGAAGCAAGAAACCGGATCAAGATCCTTCTTAAATGAC 385
 QY 361 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACCAACCAATGACCATCTGAG 420
 DB 386 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACCAACCAATGACCATCTGAG 445
 QY 421 CCATCTGGAATTTTAAATCCCTTCCACACTTGCACCAACCAATGACCATCTGAG 480
 DB 446 CCATCTGGAATTTTAAATCCCTTCCACACTTGCACCAACCAATGACCATCTGAG 505
 QY 481 CTGATTTTTCAGAGGATCTGCAACCTAGAAAGAAACCAACCAATGAGGAT 540
 DB 506 CTGATTTTTCAGAGGATCTGCAACCTAGAAAGAAACCAACCAATGAGGAT 565
 QY 541 GAGCGTGAAGATTAAGTGAATAATCATGATCAATGAAATGAGCATCCCTCTGATCCC 600
 DB 566 GAGCGTGAAGATTAAGTGAATAATCATGATCAATGAAATGAGCATCCCTCTGATCCC 625
 QY 601 CTGACATGAGAGGG-GGGCATTTAATGATGCTTCAATG 638
 DB 626 CTGACATGAGAGGGAGGATTTAATGATGCTTCAATG 664
 RESULT 208
 ADAS6090
 ID ADAS6090 standard; DNA; 1432 BP.
 AC
 XX ADAS6090;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Gene encoding human secreted protein #269.
 XX
 KM immunosuppressive; antiinflammatory; antiallergic;
 KM cyclostatic; cerebroprotective; neuroprotective; nootropic;
 KM cardiovascular; antiatherosclerotic; gene therapy;
 KM human secreted protein; immune disorder; inflammation;
 KM respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
 KM inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
 KM multiple sclerosis; ischemic brain injury; Parkinson's disease;
 KM Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
 KM triple helix formation; antisense gene therapy; forensic biology; ds;
 KM gene.
 OS Homo sapiens.
 PN WO2002102994-A2.
 PD 27-DEC-2002.
 XX 19-MAR-2002; 2002WO-US008278.
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.

XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Ruben SM;
 PI WPI; 2003-167512/16.
 XX P-PSDB; ADAS6986.
 DR
 XX New human secreted polypeptides and polynucleotides, useful for
 PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
 PT conditions, respiratory disorders, cancers, CNS disorders, or
 PT neurodegenerative disorders.
 XX
 XX Claim 21, SEQ ID NO 279; 1754bp, English.
 PS
 XX The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 CC acids encoding the polypeptides, agonists or antagonists that binds to
 CC the polypeptide, are useful in preparing diagnostic or pharmaceutical
 CC compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC hepatitis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful for molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to a gene encoding one of the polypeptide of the invention. Note: The
 CC sequence data for this patent did form part of the printed specification,
 CC but was obtained in electronic format directly from MPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;
 Query Match 98.3%; Score 627; DB 7; Length 1432;
 Best Local Similarity 99.8%; Pred. No. 2.7e-181;
 Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 ATGTGTGGGCTGCTTTTCTGAGTGCATTCATGCTGAACCTGTGCAACAGGT 60
 DB 69 ATGTGTGGGCTGCTTTTCTGAGTGCATTCATGCTGAACCTGTGCAACAGGT 128
 QY 61 GCGAAATGCTTTTAAAGTGAAGCTTATGATGAGAAAGCTCTGGAGATTAAGCATAT 120
 DB 129 GCGAAATGCTTTTAAAGTGAAGCTTATGATGAGAAAGCTCTGGAGATTAAGCATAT 188
 QY 121 GCGTGGATACCAATGAATATCTCTTCAAGGAGATGATCTTCTCCATGAGAAA 180
 DB 189 GCGTGGATACCAATGAATATCTCTTCAAGGAGATGATCTTCTCCATGAGAAA 248
 QY 181 GTTCCCAAGAGAAAGCAAGAAATTTCCCATGCTCTTCTTGGCAATGTAAACCAAGG 240
 DB 249 GTTCCCAAGAGAAAGCAAGAAATTTCCCATGCTCTTCTTGGCAATGTAAACCAAGG 308
 QY 241 GTATCATTTCTGTTGTGTGTGTACAGACCTTCAAAAATATACACCTTCTCTGTTGAG 300
 DB 309 GTATCATTTCTGTTGTGTGTGTACAGACCTTCAAAAATATACACCTTCTCTGTTGAG 368
 QY 301 GTGCAATCAGCATTAAGATGAAGCAAGAAACCGGATCAAGATCCTTCTTAAATGAC 360

DB 369 GTGCATACAGCCATAGAGTGAACAGACCGATCAACATGCTTCTTTAAATGAC 428
QY 361 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 420
DB 429 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 488
QY 421 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 480
DB 489 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 548
QY 481 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 540
DB 549 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 608
QY 541 GAGCTGAAGATTAAGTGAAGATGATGATGATGATGATGATGATGATGATGAT 600
DB 609 GAGCTGAAGATTAAGTGAAGATGATGATGATGATGATGATGATGATGATGAT 668
QY 601 CTGACATGAAGG-GGGCAATTTAAGATGCTTCAATG 638
DB 669 CTGACATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 707

RESULT 209

ADA39900 standard; cDNA; 1432 BP.

ADA39900;

20-NOV-2003 (first entry)

Human secreted protein encoding cDNA.

Human; secreted protein; cancer; hyperproliferative disorder;
rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
anemia; allergic reaction; asthma; cardiovascular disorder;
wound healing; cytotoxic; immunosuppressive; neutropenic; neuroprotective;
antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory;
vulnerable; cardiac; gene therapy; ss.

Homo sapiens.

WO2002102993-A2.

27-DEC-2002.

19-MAR-2002; 2002MO-US008123.

21-MAR-2001; 2001US-0277340P.

19-JUL-2001; 2001US-0306171P.

13-NOV-2001; 2001US-0331287P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Ruben SM;

WPI; 2003-175238/17.

New human secreted proteins and nucleic acid molecules, useful for
preparing a diagnostic or pharmaceutical composition for diagnosing,
preventing or treating cancer or other hyperproliferative disorder,
asthma, allergies or AIDS.

Claim 9; SEQ ID NO 283; 3205bp; English.

The invention relates to novel genes ADA39629-ADA40565 and proteins
ADA40566-ADA41501 for human secreted proteins, useful for preventing,
treating or ameliorating medical conditions e.g. by protein or gene
therapy. The polypeptides, nucleic acid molecules, antibodies or their
fragments, and agonists or antagonists that bind to the polypeptide are
useful for preparing a diagnostic or pharmaceutical composition for
diagnosing or treating cancer or other hyperproliferative disorder. The
polypeptides and nucleic acid molecules are also useful for detecting.

CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WFO at
CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.3%; Score 627; DB 7; Length 1432;

Best Local Similarity 99.8%; Pred. No. 2.7e-181; Mismatches 0; Indels 1; Gaps 1;

Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AATGTTGAGCTGCTCTTTTCTGTCGATGATGATGATGATGATGATGATGATGAT 60
DB 69 AATGTTGAGCTGCTCTTTTCTGTCGATGATGATGATGATGATGATGATGATGAT 128
QY 61 GCAAGAAATGCTTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 120
DB 129 GCAAGAAATGCTTTTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 188
QY 121 GCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 189 GCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
QY 181 GTTCCAAAG 240
DB 249 GTTCCAAAG 308
QY 241 GTATCATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 300
DB 309 GTATCATTTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 368
QY 301 GTGCAATCAGCTTAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 360
DB 369 GTGCAATCAGCTTAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAGATGAAG 428
QY 429 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 488
QY 421 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 480
DB 489 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 548
QY 481 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 540
DB 549 CCAATCTGGAATTTTAAATCCCTTCCACACTTGCAACCAACCATCTGTG 608
QY 541 GAGCTGAAGATTAAGTGAAGATGATGATGATGATGATGATGATGATGATGAT 600
DB 609 GAGCTGAAGATTAAGTGAAGATGATGATGATGATGATGATGATGATGATGAT 668
QY 601 CTGACATGAAGG-GGGCAATTTAAGATGCTTCAATG 638
DB 669 CTGACATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 707

RESULT 210

ADAl1489
 ID ADAl1489 standard; DNA; 1432 BP.
 AC ADAl1489;
 DT 06-NOV-2003 (first entry)
 XX Human cDNA encoding a novel secreted protein, SEQ ID NO 17.
 XX
 XX cancer; inflammation; immune disorder; neurological disorder;
 KW blood clotting disorder; food additive; food preservative;
 KW storage capability; fat content; nutritional component; ds; gene; human.
 OS Homo sapiens.
 XX US2003055236-A1.
 XX
 PD 20-MAR-2003.
 XX
 XX 14-MAR-2002; 2002US-00097065.
 PF 18-DEC-1997; 97US-0068006P.
 PR 18-DEC-1997; 97US-0068007P.
 PR 18-DEC-1997; 97US-0068008P.
 PR 18-DEC-1997; 97US-0068053P.
 PR 18-DEC-1997; 97US-0068054P.
 PR 18-DEC-1997; 97US-0068057P.
 PR 18-DEC-1997; 97US-0068064P.
 PR 18-DEC-1997; 97US-0070923P.
 PR 19-DEC-1997; 97US-0068169P.
 PR 19-DEC-1997; 97US-0068365P.
 PR 19-DEC-1997; 97US-0068367P.
 PR 19-DEC-1997; 97US-0068368P.
 PR 19-DEC-1997; 97US-0068369P.
 PR 17-DEC-1998; 98WO-US027059.
 PR 17-JUN-1999; 99US-0034595.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Moore PA, Ruben SM, Carter KC, Shi Y, Rosen CA, Soppet DR,
 PI Kyaw H, Wei Y, Florence KA, Duan DR, Florence C, Greene JM, Peng P,
 PI Ferris AM, Yu G, Janat F, Ni J;
 XX
 DR MPI: 2003-567105/53.
 DR P-PSDB; ADAl1613.
 XX
 PT New secreted HKAB724 nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 XX
 PS Claim 1, SEQ ID NO 17, 118bp; English.
 XX
 XX The invention relates to an isolated HKAB724 nucleic acid molecule. The
 CC polypeptides, nucleic acids and antibodies are useful for diagnosing a
 CC pathological condition or a susceptibility to a pathological condition,
 CC for preventing, treating, or ameliorating a medical condition, such as
 CC cancer, inflammation and other immune disorders, neurological and blood
 CC clotting disorders. The nucleic acids are also useful for chromosome
 CC identification, radiation hybrid mapping or long-range restriction
 CC mapping. The polypeptides and antibodies are useful for providing
 CC immunological probes for differential identification of the tissues
 CC immunohistochemistry assays. The polypeptide, polynucleotide, agonist or
 CC antagonist may also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content or other
 CC nutritional components. The present sequence represents cDNA encoding a
 CC novel human secreted protein. Note: The sequence data for this patent did
 CC not form part of the printed specification but was obtained in electronic
 CC format directly from USPTO at
 CC seqdata.uspto.gov.uk/sequence.html?docID=20030055236.
 CC
 CC Sequence 1432 BP; 485 A; 258 C; 252 G; 437 T; 0 U; 0 Other;

Query Match 98.3%; Score 627; DB 8; Length 1432;
 Best Local Similarity 99.8%; Pred. No. 2.7e-181;
 Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 ATGTTGGGCTGCTCTTTTTCGTCGTCATTCATGTCGTAAGTCGTCACAGGT 60
 DB 69 ATGTTGGGCTGCTCTTTTTCGTCGTCATTCATGTCGTAAGTCGTCACAGGT 128
 QY 61 GCAGAAATGCTTTAAAGTGAAGCTTAGTTCAGAAACAGCTCGGAGATTAACATAT 120
 DB 129 GCAGAAATGCTTTAAAGTGAAGCTTAGTTCAGAAACAGCTCGGAGATTAACATAT 188
 QY 121 GCCTGGATACCAATGAAGATCCTCTTCAAGCGATGATGCTTTCTCATGAGAAA 180
 DB 189 GCCTGGATACCAATGAAGATCCTCTTCAAGCGATGATGCTTTCTCATGAGAAA 248
 QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTTCTTCAATGAATCAACAGAG 240
 DB 249 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTTCTTCAATGAATCAACAGAG 308
 QY 241 GTATCATTCGTTGTTGTTAGACACCTTCAAAAATCACACCTTCTGCTGTGAG 300
 DB 309 GTATCATTCGTTGTTGTTAGACACCTTCAAAAATCACACCTTCTGCTGTGAG 368
 QY 301 GTGCATCAGCCATTAAGATGAACAGAACCGATCAACATGCTTCTTCAATGAC 360
 DB 369 GTGCATCAGCCATTAAGATGAACAGAACCGATCAACATGCTTCTTCAATGAC 428
 QY 361 CAATCTGGAATTTTAAAAATCCCTTCACACTTGCACCAACCATGAGACCATCTG 420
 DB 429 CAATCTGGAATTTTAAAAATCCCTTCACACTTGCACCAACCATGAGACCATCTG 488
 QY 421 CCATCTGATTAATTAATTTGTTGATTAATTTGATCATCATAGTTCATTCACATA 480
 DB 489 CCATCTGATTAATTAATTTGTTGATTAATTTGATCATCATAGTTCATTCACATA 548
 QY 481 CTGATTTTATCAGGATCTGCAACGTAGAAAGAAAGAAACCATCTGAAGTGAT 540
 DB 549 CTGATTTTATCAGGATCTGCAACGTAGAAAGAAAGAAACCATCTGAAGTGAT 608
 QY 541 GAGCTGAAGATTAAGTGAAGAAACATGATCATTTGAAATGGCATTCCTTGAATCC 600
 DB 609 GAGCTGAAGATTAAGTGAAGAAACATGATCATTTGAAATGGCATTCCTTGAATCC 668
 QY 601 CTGACATGAAAGG-GGGCAATTAATGATGCTTCATG 638
 DB 669 CTGACATGAAAGGAGGCAATTAATGATGCTTCATG 707
 RESULT 211
 ADD37613
 ID ADD37613 standard; cDNA; 1432 BP.
 AC ADD37613;
 DT 15-JAN-2004 (first entry)
 XX Human secreted protein encoding sequence #95.
 XX
 XX human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss.
 OS Homo sapiens.
 XX W0200290526-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 19-MAR-2002; 2002WO-US008279.
 XX
 XX 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0306171P.
 PR 13-NOV-2001; 2001US-0331287P.

by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 97 genes, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, tumors, diseases of the immune system, autoimmune deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive disorders, schizophrenia, arthritis, psoriasis, sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney disorders, digestive/endocrine disorders, infections and AIDS. The polypeptides are also useful for identifying their binding partners. The sequences shown in AAY6224 to AAY6424 represent fragments of the secreted proteins

Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

Query Match 98.2%; Score 626.6; DB 3; Length 1447;
Best Local Similarity 99.7%; Pred. No. 3.6e-181;
Matches 637; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 ATGTTGAGCTGCTTTTTCGTGAGCTGACCTGATCTGTAACCTGTAACAGGT 60
DB |||
QY 77 ATGTTGAGCTGCTTTTTCGTGAGCTGACCTGATCTGTAACCTGTAACAGGT 136
DB |||
QY 61 GCAGAAATGCTTTTAAAGTGAAGTGAATGATGAGAAAGCTCTGGAGATTAAGCATAT 120
DB |||
QY 137 GCAGAAATGCTTTTAAAGTGAAGTGAATGATGAGAAAGCTCTGGAGATTAAGCATAT 196
DB |||
QY 121 GCTGGAGATACCAATGAATATCTCTCAAGGAGTGTAGCTTTCTCCAGAGAAA 180
DB |||
QY 197 GCTGGAGATACCAATGAATATCTCTCAAGGAGTGTAGCTTTCTCCAGAGAAA 256
DB |||
QY 181 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTTCAATGTAACCCAGAG 240
DB |||
QY 257 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTTCAATGTAACCCAGAG 316
DB |||
QY 241 GATATCTGCTGTTTGTGTGACAGCTTCAAAAATGACACCTCTGCTGTTGAG 300
DB |||
QY 317 GATATCTGCTGTTTGTGTGACAGCTTCAAAAATGACACCTCTGCTGTTGAG 376
DB |||
QY 301 GTGCAATGACCTTAAGAAATGAAACCGGATGAAACCTCTTCTTAAATGAC 360
DB |||
QY 377 GTGCAATGACCTTAAGAAATGAAACCGGATGAAACCTCTTCTTAAATGAC 436
DB |||
QY 361 GAACTCTGAAATTTTAAATCCCTTCACTGACACCCATGAGACCATCTGTG 420
DB |||
QY 437 GAACTCTGAAATTTTAAATCCCTTCACTGACACCCATGAGACCATCTGTG 496
DB |||
QY 421 CCCATCTGATTTATTTATTTGTTGATATTTTTCATCATGATGTAATGACATA 480
DB |||
QY 497 CCCATCTGATTTATTTATTTGTTGATATTTTTCATCATGATGTAATGACATA 556
DB |||
QY 481 CTGATTTTATTCAGGAGATCTGGCAAGTGAAGAAAGAAACCAATCTGAAGTGAAT 540
DB |||
QY 557 CTGATTTTATTCAGGAGATCTGGCAAGTGAAGAAAGAAACCAATCTGAAGTGAAT 616
DB |||
QY 541 GAGCTGAAGATTAAGTGAAGAAATGATCAATGAAATGAGCATCCCTCTGATCCC 600
DB |||
QY 617 GAGCTGAAGATTAAGTGAAGAAATGATCAATGAAATGAGCATCCCTCTGATCCC 676
DB |||
QY 601 CTGAGCATGAGAGG-GGGCATATTATGATGCTTCAAG 638
DB |||
QY 677 CTGAGCATGAGAGGAGGAGATATTATGATGCTTCAAG 715
DB |||
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RESULT 213

AD811650
ID ADE11650 standard; cDNA, 1447 BP.

AC ADE11650;

XX 29-JAN-2004 (first entry)

XX Human secreted polypeptide cDNA #12.

XX Secreted protein; cancer; liver disorder; hepatitis; neural disorder;
KW Alzheimer's disease; human; ss; gene.

XX Synthetic.
OS Homo sapiens.

PN US2003100051-A1.

XX 29-MAY-2003.

PF 10-SEP-2001; 2001US-00948783.

PR 12-MAY-1998; 98US-0085093P.

PR 12-MAY-1998; 98US-0085094P.

PR 12-MAY-1998; 98US-0085105P.

PR 12-MAY-1998; 98US-0085180P.

PR 18-MAY-1998; 98US-0085906P.

PR 18-MAY-1998; 98US-0085920P.

PR 18-MAY-1998; 98US-0085921P.

PR 18-MAY-1998; 98US-0085922P.

PR 18-MAY-1998; 98US-0085923P.

PR 18-MAY-1998; 98US-0085924P.

PR 18-MAY-1998; 98US-0085925P.

PR 18-MAY-1998; 98US-0085927P.

PR 18-MAY-1998; 98US-0085928P.

PR 06-MAY-1999; 99MO-US009847.

PR 10-NOV-1999; 99US-00437658.

PR 11-SEP-2000; 2000US-0231846P.

PR 28-JUN-2001; 2001US-00892877.

XX (RUBEN S. M.

XX (FLORENCE K. A.

XX (NI J.

XX (ROSE/ ROSEN C. A.

XX (CART/ CARTER K. C.

XX (MOOR/ MOORE P. A.

XX (OLSE/ OLSEN H. S.

XX (SHI/ SHI Y.

XX (YOUN/ YOUNG P. B.

XX (WEI/ WEI Y.

XX (BREM/ BREMER L. A.

XX (SOP/ SOPP D. R.

XX (LAFL/ LAFLEUR D. W.

XX (ENDR/ ENDRESS G. A.

XX (BENR/ BENNER R.

XX (BIRS/ BIRSE C. B.

XX Ruben SM, Florence KA, Ni J, Rosen CA, Carter KC, Moore PA,

XX Olsen HS, Shi Y, Young PB, Wei Y, Bremer LA, Soppet DR, Lafleur DW,

XX Endress GA, Ebner R, Birse CE;

XX WPI; 2003-801210/75.

XX New nucleic acid molecule, useful for preparing a medicament for

XX preventing, treating or ameliorating a medical condition e.g. cancer,

XX liver disorders or neural disorders.

XX Claim 1; SEQ ID NO 22; 453bp; English.

XX The invention relates to human secreted polypeptides and the

XX polynucleotides encoding them. The sequences are useful for preparing

XX medicaments for preventing, treating or ameliorating medical conditions

XX e.g., cancer, liver disorders such as hepatitis or neural disorders such

XX as Alzheimer's disease. This sequence represents cDNA encoding a human

XX secreted polypeptide of the invention.

XX Sequence 1447 BP; 488 A; 262 C; 256 G; 439 T; 0 U; 2 Other;

XX SQ

Query Match 98.2%; Score 626.6; DB 9; Length 1447;

Best Local Similarity 99.7%; Pred. No. 3.6e-181;
Matches 637; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTGTGGCTGCTCTTTTTCGTGTAATCCATTCATGCTGAACCTGTCAACAGGT 60
DB 77 ATGTGTGGCTGCTCTTTTTCGTGTAATCCATTCATGCTGAACCTGTCAACAGGT 136
QY 61 GCAGAAATGCTTTTAAAGTGAAGCTTATGATCAAGCTGTGGAGAAAGCAATAT 120
DB 137 GCAGAAATGCTTTTAAAGTGAAGCTTATGATCAAGCTGTGGAGAAAGCAATAT 196
QY 121 GCTGGGATACCAATGAAGATACCTCTCAAGCGATGTAGCTTCTCCATGAGAAA 180
DB 197 GCTGGGATACCAATGAAGATACCTCTCAAGCGATGTAGCTTCTCCATGAGAAA 256
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCTTCTTCAATGTAACCAAGAG 240
DB 257 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCTTCTTCAATGTAACCAAGAG 316
QY 241 GTATCATTTCTGTTGTGTGTTACGAGCCCTTCAAAAATGCAACCTTCTGCTGGAG 300
DB 317 GTATCATTTCTGTTGTGTGTTACGAGCCCTTCAAAAATGCAACCTTCTGCTGGAG 376
QY 301 GTGCAATCAGCCATTAAGATGAAGAACCGGATCAACATGCTTCTTCTTAATGAC 360
DB 377 GTGCAATCAGCCATTAAGATGAAGAACCGGATCAACATGCTTCTTCTTAATGAC 436
QY 361 CAAACTCTGAAATTTTAAATCCCTTCAACACTTGCACCAACCCATGACCATCTGTG 420
DB 437 CAAACTCTGAAATTTTAAATCCCTTCAACACTTGCACCAACCCATGACCATCTGTG 496
QY 421 CCGATCTGATTTATTTATTTGTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 480
DB 497 CCGATCTGATTTATTTATTTGTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 556
QY 481 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAAAGAAACCATCTGAATGAT 540
DB 557 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAAAGAAACCATCTGAATGAT 616
QY 541 GACCTGAAGATTAAGTGAAGAAACATGATCAACATGAAATGCAATGCAATGCAATGCAATGCAAT 600
DB 617 GACCTGAAGATTAAGTGAAGAAACATGATCAACATGAAATGCAATGCAATGCAATGCAATGCAAT 676
QY 601 CTGCAATGAAGAGG-GGGCATATTAAGATGCTTCAAG 638
DB 677 CTGCAATGAAGAGG-GGGCATATTAAGATGCTTCAAG 715

RESULT 214
AB278127
ID AB278127 standard; cDNA; 1345 BP.
XX
AC AB278127;
XX
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related coding sequence. 156P1D4.
XX
KM Human; cytosolic; vaccine; cancer; immune response; gene; ss.
XX
OS Homo sapiens.
XX
PN W0200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002MO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
XX
PR 10-APR-2001; 2001US-0283112P.
XX
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
XT Jakovlevs A, Challita-Bid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;

XX WP1: 2003-075555/07.
DR P-PSDB; ABR01796.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 26; Fig 2C; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278166 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. 74P3B3 maps
CC to chromosome 8p21.3-p22, 83P4B8 maps to chromosome 15q25.1, 109P1D4 maps
CC to chromosome Xq21.3, 151P1C7A maps to chromosome 10q11.2, 151P4B11 maps
CC to chromosome 11q13.3-q13.5, 154P2A8 maps to chromosome 3q24, 156P1D4
CC maps to chromosome Xp22.3, 156P5C12 maps to chromosome 2p13.1-p12,
CC 159P2B5 maps to chromosome 7p15.1, 161P2B7A maps to chromosome 3q25-q26,
CC 179P3G7 maps to chromosome 12q12-q13, 184P3G10 maps to chromosome
CC 19p13.1, 184P3G10 maps to chromosome 2p12, 185P2C9 maps to chromosome
CC 18p11.22, 185P3G10 maps to chromosome 17q21, 186P1H9 maps to chromosome
CC 7q21.3-q22.1, 187P3F2 maps to chromosome 3p14.2 and 192P2G7 maps to
CC chromosome 22q13.2-q13.31
XX
SQ Sequence 1345 BP; 435 A; 251 C; 241 G; 418 T; 0 U; 0 Other;
Query Match 98.0%; Score 625.4; DB 7; Length 1345;
Best Local Similarity 99.7%; Pred. No. 8.2e-181;
Matches 637; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 ATGTGTGGCTGCTCTTTTTCGTGTAATCCATTCATGCTGAACCTGTCAACAGGT 60
DB 24 ATGTGTGGCTGCTCTTTTTCGTGTAATCCATTCATGCTGAACCTGTCAACAGGT 83
QY 61 GCAGAAATGCTTTTAAAGTGAAGCTTATGATCAAGCTGTGGAGAAAGCAATAT 120
DB 84 GCAGAAATGCTTTTAAAGTGAAGCTTATGATCAAGCTGTGGAGAAAGCAATAT 143
QY 121 GCTGGGATACCAATGAAGATACCTCTCAAGCGATGTAGCTTCTCCATGAGAAA 180
DB 144 GCTGGGATACCAATGAAGATACCTCTCAAGCGATGTAGCTTCTCCATGAGAAA 203
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCTTCTTCAATGTAACCAAGAG 240
DB 204 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCTTCTTCAATGTAACCAAGAG 263
QY 241 GTATCATTTCTGTTGTGTGTTACGAGCCCTTCAAAAATGCAACCTTCTGCTGGAG 300
DB 264 GTATCATTTCTGTTGTGTGTTACGAGCCCTTCAAAAATGCAACCTTCTGCTGGAG 323
QY 301 GTGCAATCAGCCATTAAGATGAAGAACCGGATCAACATGCTTCTTCTTAATGAC 360
DB 324 GTGCAATCAGCCATTAAGATGAAGAACCGGATCAACATGCTTCTTCTTAATGAC 383
QY 361 CAAACTCTGAAATTTTAAATCCCTTCAACACTTGCACCAACCCATGACCATCTGTG 420
DB 384 CAAACTCTGAAATTTTAAATCCCTTCAACACTTGCACCAACCCATGACCATCTGTG 443
QY 421 CCGATCTGATTTATTTATTTGTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 480
DB 444 CCGATCTGATTTATTTATTTGTGTGATTTTGTGATTTTGTGATTTTGTGATTTTGTGAT 503
QY 481 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAAAGAAACCATCTGAATGAT 540
DB 504 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAAAGAAACCATCTGAATGAT 563

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QY 541 GACGCTGAAGATAGTGTGTAACAAATGATCACAATTGAAATGCAATCCCTCTGATGCC 600
DB 544 GACGCTGAAGATAGTGTGTAACAAATGATCACAATTGAAATGCAATCCCTCTGATGCC 623
QY 601 CTGACATGAGAGG-GGGCATATTATGATGCTTCATG 638
DB 624 CTGACATGAGAGGAGGCATATTATGATGCTTCATG 662

RESULT 215
AAV40540 standard; cDNA; 1401 BP.
AAV40540;
AAV40540;
09-NOV-1998 (first entry)
Homo sapiens secreted protein clone AM42_3.
Clone; secreted protein; ds.
Homo sapiens.
Key Location/Qualifiers
CDS 71..739
FT /*tag= a
FT /note= "secreted protein"
XN MO9832853-A2.
XX 30-JUL-1998.
XX 23-JAN-1998; 98MO-US001396.
XX 24-JAN-1997; 97US-00788789.
XX (GENY ) GENETICS INST INC.
XX PI Jacobs K, McCoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
PI Spaulding V, Agoetino MJ;
XX MPI; 1998-427949/36.
XX P-PSDB; AAW29670.
XX New isolated polynucleotide(s) and secreted proteins - isolated from
XX human foetal kidney, adult brain, adult salivary gland, foetal brain and
XX adult testes cDNA libraries.
XX Claim 16; Page 64-65; 109pp; English.
XX The sequence is that of encoding a secreted protein. Such a protein can
XX have biological activities, e.g. nutritional activity, cytokine and cell
XX proliferation/differentiation activity, immune stimulating or suppressing
XX activity, haematopoiesis regulating activity, tissue growth activity,
XX activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, cadherin/tumour invasion suppressor activity, tumour inhibition
XX activity, and other activities
XX Sequence 1401 BP; 458 A; 258 C; 251 G; 434 T; 0 U; 0 Other;
XX
Query Match 98.0%; Score 625.4; DB 2; Length 1401;
Best Local Similarity 99.7%; Pred. No. 8.3e-181;
Matches 637; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 ATGTTGTGGCTGCTCTTTTCTGTCGACCTGATTCATGCTGCACTGTCAACCAAGGT 60
DB 71 ATGTTGTGGCTGCTCTTTTCTGTCGACCTGATTCATGCTGCACTGTCAACCAAGGT 130
QY 61 GCAGAAATGCTTTTAAAGTGAAGCTTACTATCAGAACGCTCTGGAGATTAAGCATAT 120
DB 131 GCAGAAATGCTTTTAAAGTGAAGCTTACTATCAGAACGCTCTGGAGATTAAGCATAT 190

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QY 121 GCCTGGATACCAATGAAGATACCTCTTCAAGCGATGAGCTTCTTCATGAGAAA 180
DB 191 GCCTGGATACCAATGAAGATACCTCTTCAAGCGATGAGCTTCTTCATGAGAAA 250
QY 181 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCCTTCTTGCAATGAACCCGAGG 240
DB 251 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCCTTCTTGCAATGAACCCGAGG 310
QY 241 GTATCATTCGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300
DB 311 GTATCATTCGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 370
QY 301 GTGCAATCAGCCATGAAGATGAAGCAAGAACCGATCAAGATGCTTCTTCTTAAATGAC 350
DB 371 GTGCAATCAGCCATGAAGATGAAGCAAGAACCGATCAAGATGCTTCTTCTTAAATGAC 430
QY 361 CAACTCTGGAATTTTAAATATCCCTTCCACACTTGCACACCCCATGAGACCATCTG 420
DB 431 CAACTCTGGAATTTTAAATATCCCTTCCACACTTGCACACCCCATGAGACCATCTG 490
QY 421 CCATCTGATATTATATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 480
DB 491 CCATCTGATATTATATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 550
QY 481 CTGATTTTATCAGGATCTGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 540
DB 551 CTGATTTTATCAGGATCTGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 610
QY 541 GACGCTGAAGATAGTGTGTAACAAATGATCACAATTGAAATGCAATCCCTCTGATGCC 600
DB 611 GACGCTGAAGATAGTGTGTAACAAATGATCACAATTGAAATGCAATCCCTCTGATGCC 670
QY 601 CTGACATGAGAGG-GGGCATATTATGATGCTTCATG 638
DB 671 CTGACATGAGAGGAGGCATATTATGATGCTTCATG 709

RESULT 216
AAK19983
ID AAK19983 standard; cDNA; 848 BP.
XX AAK19983;
XX 16-JUN-1999 (first entry)
XX Human secreted protein 5' EST SBQ ID NO:27.
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX Homo sapiens.
XX MO9906439-A2.
XX 11-FEB-1999.
XX 31-JUL-1998; 98MO-IB001233.
XX 01-AUG-1997; 97US-00904468.
XX (GENST ) GENSET.
XX Dumas Milne Edwards J, Duclert A, Lacroix B;
XX MPI; 1999-153700/13.
XX P-PSDB; AAY04156.
XX New nucleic acids encoding human secreted proteins - obtained from cDNA
PT

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PT Libraries derived from liver, lung, large intestine, colon, thyroid and
PT pancreas tissue.

XX Example 28; Page 157-158; 398bp; English.

CC AAX40251 to AAX40397 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY11533 to
CC AAY11679, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC present sequence represents a 5' EST from an example of the present
CC invention

SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181; Mismatches 0; Indels 1; Gaps 1;

Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTTGGGCTGCTCTTTTCTGAGTGCATTCATGCTGAACCTGCTCAACAGGT 60

DB 32 ATGTTGGGCTGCTCTTTTCTGAGTGCATTCATGCTGAACCTGCTCAACAGGT 91

QY 61 GCAGAAAATGCTTTTAAAGTGAAGTATGATGACAGCTCTGGAGATTAACATAT 120

DB 92 GCAGAAAATGCTTTTAAAGTGAAGTATGATGACAGCTCTGGAGATTAACATAT 151

QY 121 GCCCTGGATTAACAGTAAGTAAGTAAAGGAGTGAAGCTTTCCATGAGAAA 180

DB 152 GCCCTGGATTAACAGTAAGTAAGTAAAGGAGTGAAGCTTTCCATGAGAAA 211

QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTCTACTTGTGATGATACCAAGG 240

DB 212 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTCTACTTGTGATGATACCAAGG 271

QY 241 GTATCATTTCTGTTTGTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 300

DB 272 GTATCATTTCTGTTTGTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 331

QY 301 GTGCAATCAGCATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 360

DB 332 GTGCAATCAGCATTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 391

QY 361 CAAACTCTGAATTTTAAATCCCTTCAACTTGAACCAACCAACCAACCAACCA 420

DB 392 CAAACTCTGAATTTTAAATCCCTTCAACTTGAACCAACCAACCAACCAACCA 451

QY 421 CCCATCTGATTAATTAATTTGTTGTAATTTTGCATCATCAATGTTCAATTGCACTA 480

DB 452 CCCATCTGATTAATTAATTTGTTGTAATTTTGCATCATCAATGTTCAATTGCACTA 511

QY 481 CTGATTTTAACAGGATCTGCAACGTAGAAAGAAAGAAAGAAAGAAAGAAAGTAT 540

DB 512 CTGATTTTAACAGGATCTGCAACGTAGAAAGAAAGAAAGAAAGAAAGAAAGTAT 571

QY 541 GACCTGAAGATTAAGTGAAGAAACATGATCAATTTGAAATGGATCCCTCTGATCC 600

DB 572 GACCTGAAGATTAAGTGAAGAAACATGATCAATTTGAAATGGATCCCTCTGATCC 631

QY 601 CTGACATGAAGGG-GGGCATTTATATGATGCTTCAAG 638

DB 632 CTGACATGAAGGGGCGCATTTATATGATGCTTCAAG 670

RESULT 217

AAX39430

XX AAX39430 standard; DNA; 848 BP.

AC AAX39430;

DT 21-JUN-1999 (first entry)

DE Human secreted protein 5' EST SEQ ID NO: 27.

XX

OS

XX Homo sapiens.

XX MO9906551-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98W0-1B001235.

XX 01-AUG-1997; 97US-00905133.

XX (GBST) GENSET.

XX Dunas Milne Edwards J, Duclert A, Lacroix B;

XX MPI: 1999-153781/13.

XX P-PSDB; AAM93620, AAY11373.

XX New nucleic acids encoding human secreted - proteins obtained from cDNA

XX PT libraries prepared from substantia nigra, cerebellum, surreals and fetal

XX PT brain tissue.

XX Example 28; Page 157-158; 434pp; English.

XX AAX39440 to AAX39597 represent 5' expressed sequence tags (ESTs) for

XX human secreted proteins, and encode the proteins given in AAY11574 to

XX AAY11571, respectively. The proteins given represent the signal peptide

XX and an N-terminal fragment of a secreted protein. The nucleic acid

XX sequences can be used for producing secreted human gene products. They

XX can also be used to develop products for diagnosis and therapy. The

XX proteins obtained may have cytokine activity, cell

XX proliferation/differentiation activity, haematopoiesis regulating

XX activity, tissue growth regulating activity, reproductive hormone

XX regulating activity, chemotactic/chemokinetic activity, haemostatic and

XX thrombolytic activity, receptor/ligand activity, anti-inflammatory

XX activity, tumour inhibition activity or other activities. The products

XX can be used in forensic, gene therapy and chromosome mapping procedures.

XX The sequences can also be used for obtaining corresponding promoter

XX sequences. The nucleic acids encoding the signal peptide can be used for

XX directing extracellular secretion of a polypeptide or the insertion of a

XX polypeptide into a membrane, or importing a polypeptide into a cell. This

XX sequence encodes the human 5' EST secreted proteins represented in

XX AAM93620 and AAY11373

XX SQ

Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181; Mismatches 0; Indels 1; Gaps 1;

Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTTGGGCTGCTCTTTTCTGAGTGCATTCATGCTGAACCTGCTCAACAGGT 60

DB 32 ATGTTGGGCTGCTCTTTTCTGAGTGCATTCATGCTGAACCTGCTCAACAGGT 91

QY 61 GCAGAAAATGCTTTAAAGTACTTACTATCAGAACGCTCTGGAGATAAAGCATAT 120
DB 92 GCAGAAAATGCTTTAAAGTACTTACTATCAGAACGCTCTGGAGATAAAGCATAT 151
QY 121 GCTTGGATCCCAATGAAGAAATACCTCTTCAAGAGCATGTGCTTCTCCATGAGAAA 180
DB 152 GCTTGGATCCCAATGAAGAAATACCTCTTCAAGAGCATGTGCTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCCATGCTCTTCTTGCATATGTAACCCAGAG 240
DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCCATGCTCTTCTTGCATATGTAACCCAGAG 271
QY 241 GTATCATCTGTGTTGTGTGTTACAGACCTTCACAAAATACACCCCTTCCTGTGTAG 300
DB 272 GTATCATCTGTGTTGTGTGTTACAGACCTTCACAAAATACACCCCTTCCTGTGTAG 331
QY 301 GTGCATCAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAAATGAC 360
DB 332 GTGCATCAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAAATGAC 391
QY 361 CAAACTCTGGAATTTTAAATAATCCCTTCACACTGACCAACCAATGACCATCTGTG 420
DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTGACCAACCAATGACCATCTGTG 451
QY 421 CCATCTGGAATTTTAAATAATGCTGTGATATTTTGCATATGTAATGCAATGCACTA 480
DB 452 CCATCTGGAATTTTAAATAATGCTGTGATATTTTGCATATGTAATGCAATGCACTA 511
QY 481 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAACCAAGACCATCTGAATGAT 540
DB 512 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAACCAAGACCATCTGAATGAT 571
QY 541 GACGCTGAAGATTAAGTGAAGAACATGATCACAATGGAATGCAATGCTGTATGCC 600
DB 572 GACGCTGAAGATTAAGTGAAGAACATGATCACAATGGAATGCAATGCTGTATGCC 631
QY 601 CTGACATGAAGAGG-GGGCATATTAATGATGCTTCATG 638
DB 632 CTGACATGAAGAGGAGGCAATTAATGATGCTTCATG 670

RESULT 218
AAK41369
ID AAK41369 standard; cDNA; 848 BP.
XX
AC AAK41369;
XX
DT 22-JUN-1999 (first entry)
XX
DE Extended cDNA obtained from 5' EST. SEQ ID NO: 27 from WO 9906553.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; antiinflammatory; tumour inhibition; antitumour; de.
XX
OS Homo sapiens.
XX
PN WO9906553-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-1B001237.
XX
PR 01-AUG-1997; 97US-00905051.
XX
PA (GBST) GENSSET.
XX
PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX
DR WPI, 1999-153783/13.

DR P-PSDB; AAY12520.
XX
PT New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries derived from umbilical cord, lymph ganglia, lymphocytes and
PT placental tissue.
XX
PS Example 28; Page 156-157; 411pp; English.
XX
SS The patent relates to sequences of 5' ESTs derived from mRNAs encoding
CC secreted proteins. The nucleic acid sequences can be used for producing
CC secreted human gene products. They can also be used to develop products
CC for diagnosis and therapy. The proteins obtained may have cytokine
CC activity, cell proliferation/differentiation activity, haematopoiesis
CC regulating activity, tissue growth regulating activity, reproductive
CC hormone regulating activity, chemotactic/chemokinetic activity,
CC haemostatic and thrombolytic activity, receptor/ligand activity,
CC antiinflammatory activity, tumour inhibition activity or other
CC activities. The products can be used in forensic, gene therapy and
CC chromosome mapping procedures. The sequences can also be used for
CC obtaining corresponding promoter sequences. The nucleic acids encoding
CC the signal peptide can be used for directing extracellular secretion of a
CC polypeptide or the insertion of a polypeptide into a membrane, or
CC importing a polypeptide into a cell
XX
SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;
XX
Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8, 7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGTTGAGCTGCTCTTTTCTGTGACTGCTCATTCATGCTGTAACCTGTCAACAGT 60
DB 32 ATGTTGAGCTGCTCTTTTCTGTGACTGCTCATTCATGCTGTAACCTGTCAACAGT 91
QY 61 GCAAGAAAATGCTTTTAAAGTGAAGTCTTATGAGAAAGCTCTGGAGATAAAGCATAT 120
DB 92 GCAAGAAAATGCTTTTAAAGTGAAGTCTTATGAGAAAGCTCTGGAGATAAAGCATAT 151
QY 121 GCTTGGATCCCAATGAAGAAATACCTCTTCAAGAGCATGTGCTTCTCCATGAGAAA 180
DB 152 GCTTGGATCCCAATGAAGAAATACCTCTTCAAGAGCATGTGCTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCCATGCTCTTCTTGCATATGTAACCCAGAG 240
DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCCATGCTCTTCTTGCATATGTAACCCAGAG 271
QY 241 GTATCATCTGTGTTGTGTGTTACAGACCTTCACAAAATACACCCCTTCCTGTGTAG 300
DB 272 GTATCATCTGTGTTGTGTGTTACAGACCTTCACAAAATACACCCCTTCCTGTGTAG 331
QY 301 GTGCATCAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAAATGAC 360
DB 332 GTGCATCAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAAATGAC 391
QY 361 CAAACTCTGGAATTTTAAATAATCCCTTCACACTGACCAACCAATGACCATCTGTG 420
DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTGACCAACCAATGACCATCTGTG 451
QY 421 CCATCTGGAATTTTAAATAATGCTGTGATATTTTGCATATGTAATGCAATGCACTA 480
DB 452 CCATCTGGAATTTTAAATAATGCTGTGATATTTTGCATATGTAATGCAATGCACTA 511
QY 481 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAACCAAGACCATCTGAATGAT 540
DB 512 CTGATTTTATCAGGATCTGCAACGTAGAGAAAGAACCAAGACCATCTGAATGAT 571
QY 541 GACGCTGAAGATTAAGTGAAGAACATGATCACAATGGAATGCAATGCTGTATGCC 600
DB 572 GACGCTGAAGATTAAGTGAAGAACATGATCACAATGGAATGCAATGCTGTATGCC 631
QY 601 CTGACATGAAGAGG-GGGCATATTAATGATGCTTCATG 638
DB 632 CTGACATGAAGAGGAGGCAATTAATGATGCTTCATG 670

XX Example 28; Page 141-142; 244pp; English.

CC This sequence represents a portion of a nucleic acid sequence of the
CC invention. The invention relates to 70 nucleic acids encoding human
CC secreted proteins. The extended cDNAs (or genomic DNAs obtainable from
CC them) may be used to prepare PCR primers and probes. These are useful for
CC forensic matching or positive identification by DNA sequencing. They may
CC also be used in alternative fingerprint identification techniques.
CC Antibodies against the proteins encoded by the extended cDNAs are useful
CC in identification of tissue types or cell species, as well as identifying
CC tissue specific soluble proteins. The sequences can be used for
CC chromosome mapping and identification of genes associated with hereditary
CC diseases or drug response. Signal sequences from the cDNAs can be used in
CC construction of secretion vectors. Other sequences derived from the
CC extended cDNAs can be used to clone upstream genomic DNA sequences
CC including promoters. This is in turn useful for identifying proteins that
CC interact with promoter sequences. Some of the proteins may be useful in
CC diagnosing and treating several disorders including, but not limited to:
CC cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders,
CC autoimmune diseases, and rheumatic diseases, embryogenic disorders,
CC hypertension, renal injury, amino acidurias, hypoglycaemia, male rat
CC infertility and myopathies

CC Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;
Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

1 ATGTTGGCTGCTCTTTTTCGAGTCTGACCTGATTCAGTCACTGTCACAGGT 60
2 ATGTTGGCTGCTCTTTTTCGAGTCTGACCTGATTCAGTCACTGTCACAGGT 91
61 GCAGAAATGCTTTTAAAGTGAAGTATGATGATGATGATGATGATGATGAT 120
92 GCAGAAATGCTTTTAAAGTGAAGTATGATGATGATGATGATGATGATGAT 151
121 GCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
152 GCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 211
181 GTTCCCAAG 240
212 GTTCCCAAG 271
241 GTATCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 300
272 GTATCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 331
301 GTGCAATCGCCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
332 GTGCAATCGCCATGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391
361 CAAACCTGGAGATTTTAAATATCCCTCCAGCTGACCCAGCCAGCCAGCTG 420
392 CAAACCTGGAGATTTTAAATATCCCTCCAGCTGACCCAGCCAGCCAGCTG 451
421 CCAATCTGATATTAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 480
452 CCAATCTGATATTAATATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 511
481 CTGATTTTATCGAGATCTGGCAAGTATGAGAGAGAGAGAGAGAGAGAGAG 540
512 CTGATTTTATCGAGATCTGGCAAGTATGAGAGAGAGAGAGAGAGAGAGAG 571
541 GAGGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
572 GAGGCTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 631
601 CTGACATGAG 638
632 CTGACATGAG 670

RESULT 221

AAK26672

ID AAK26672 standard; RNA; 848 BP.

AAK26672;

18-JUN-1999 (first entry)

DE Extended cDNA derived from a 5' EST encoding a secreted protein.

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;

KW forensic; gene therapy; chromosome mapping; signal peptide;

KW upstream regulatory sequence; cytokine activity; cell proliferation;

KW differentiation; haematopoiesis regulation; tissue growth regulation;

KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;

KW thrombolytic; anti-inflammatory; tumour inhibition; ss.

OS Homo sapiens.

PN MO9906554-A2.

PD 11-FEB-1999.

PF 31-JUL-1998; 98MO-IB001238.

PR 01-AUG-1997; 97US-00905134.

DR WPI; 1999-153784/13.

DR P-PSDB; AAY01594.

PT New nucleic acids encoding human secreted proteins - obtained from cDNA

PT libraries prepared from kidney, fetal kidney, dystrophic muscle, muscle

PT and heart tissue.

PS Example 28; Page 160-161; 622pp; English.

XX The present sequence represents an extended cDNA sequence derived from a

CC 5' EST encoding a secreted protein. The specification describes 5'

CC expressed sequence tags (ESTs, see AAY0826-X41093) for human secreted

CC proteins (see AAY01602 and AAY11994-Y12260). The proteins given represent

CC the signal peptide and an N-terminal fragment of a secreted protein. The

CC nucleic acid sequences can be used for producing secreted human gene

CC products. They can also be used to develop products for diagnosis and

CC therapy. The proteins obtained may have cytokine activity, cell

CC proliferation/differentiation activity, haematopoiesis regulating

CC activity, tissue growth regulating activity, reproductive hormone

CC regulatory activity, chemotactic/chemokinetic activity, haemostatic and

CC thrombolytic activity, receptor/ligand activity, anti-inflammatory

CC activity, tumour inhibition activity or other activities. The products

CC can be used in forensic, gene therapy and chromosome mapping procedures.

CC The sequences can also be used for obtaining corresponding promoter

CC sequences. The nucleic acids encoding the signal peptide can be used for

CC directing extracellular secretion of a polypeptide or the insertion of a

CC polypeptide into a membrane, or importing a polypeptide into a cell

SO Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

1 ATGTTGGCTGCTCTTTTTCGAGTCTGACCTGATTCAGTCACTGTCACAGGT 60
32 ATGTTGGCTGCTCTTTTTCGAGTCTGACCTGATTCAGTCACTGTCACAGGT 91
61 GCAGAAATGCTTTTAAAGTGAAGTATGATGATGATGATGATGATGATGAT 120

Db 632 CTGACATGAGGAGGAGCATATTATGATGCTTCATG 670

RESULT 223

AAK51449
ID AAK51449 standard; DNA; 848 BP.

XX AAK51449;

DT 21-JUN-1999 (first entry)

XX Human secreted protein 5' EST SEQ ID NO. 27.

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemokine; chemokine; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition; ds.

XX Homo sapiens.

XX WO9906549-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-IB001231.

XX 01-AUG-1997; 97US-00905279.

XX (BEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Lacroix B;

XX WPI; 1999-153779/13.

XX P-PSDB; AAY12679, AAY12680.

XX New nucleic acids encoding human secreted proteins - obtained from cDNA

XX libraries derived from testis, ovary, uterus and spleen tissue.

XX Example 28; Page 159-160; 522pp; English.

XX AAK51459 to AAK51691 represent 5' expressed sequence tags (ESTs) for
XX human secreted proteins, and encode the proteins given in AAY12681 to
XX AAY12913, respectively. The proteins given represent the signal peptide
XX and an N-terminal fragment of a secreted protein. The nucleic acid
XX sequences can be used for producing secreted human gene products. They
XX can also be used to develop products for diagnosis and therapy. The
XX proteins obtained may have cytokine activity, cell
XX proliferation/differentiation activity, haematopoiesis regulating
XX activity, tissue growth regulating activity, reproductive hormone
XX regulating activity, chemotactic/chemokinetic activity, haemostatic and
XX thrombolytic activity, receptor/ligand activity, anti-inflammatory
XX activity, tumour inhibition activity or other activities. The products
XX can be used in forensic, gene therapy and chromosome mapping procedures.
XX The sequences can also be used for obtaining corresponding promoter
XX sequences. The nucleic acids encoding the signal peptide can be used for
XX directing extracellular secretion of a polypeptide or the insertion of a
XX polypeptide into a membrane, or importing a polypeptide into a cell. This
XX sequence represents an oligonucleotide used in an example in the
XX invention, to the isolate the 5' EST sequences of the invention

XX Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

XX Query Match 98.0%; Score 625; DB 2; Length 848;

XX Best Local Similarity 99.2%; Pred. No. 8.7e-181;

XX Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

XX 1 ATGTTGTCGCTCTCTTTTTCGAGCTGACATTCAGCTGAACCTGTCAACAGGT 60

XX 32 ATGTTGTCGCTCTCTTTTTCGAGCTGACATTCAGCTGAACCTGTCAACAGGT 91

Qy 61 GCAGAAAATGCTTTAAAGTGAAGCTTAGTACAGAAAGCTCTGGAGATTAAGCATAT 120

Db 92 GCAGAAAATGCTTTAAAGTGAAGCTTAGTACAGAAAGCTCTGGAGATTAAGCATAT 151

Qy 121 GCTGGATTCATTAAGATACCTTTCAAGCCATGTGATGTTTCTCCATGAGAAA 180

Db 152 GCTGGATTCATTAAGATACCTTTCAAGCCATGTGATGTTTCTCCATGAGAAA 211

Qy 181 GTTCCAG 240

Db 212 GTTCCAG 271

Qy 241 GTATCATTCGTTGTGTGTTACAGACCTTCAAAAATATCAACCTTCTGCTGTGAG 300

Db 272 GTATCATTCGTTGTGTGTTACAGACCTTCAAAAATATCAACCTTCTGCTGTGAG 331

Qy 301 GTGCAATCAGCCATTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360

Db 332 GTGCAATCAGCCATTAAGATGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391

Qy 361 CAAACCTGGAATTTTAAAAATCCCTTCCACCTTGACACCAACCATGAGCCATCTG 420

Db 392 CAAACCTGGAATTTTAAAAATCCCTTCCACCTTGACACCAACCATGAGCCATCTG 451

Qy 421 CCATCTGATTTATTAATTTGTGTGATATTTTGCATCATATGATGCAATGCACTA 480

Db 452 CCATCTGATTTATTAATTTGTGTGATATTTTGCATCATATGATGCAATGCACTA 511

Qy 481 CTGATTTATCAGGATCTGCGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 540

Db 512 CTGATTTATCAGGATCTGCGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 571

Qy 541 GAGCTGAATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

Db 572 GAGCTGAATTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631

Qy 601 CTGACATGAAGAGG-GGGCATATTATGATGATGCTTCATG 638

Db 632 CTGACATGAAGAGGAGGATATTATGATGCTTCATG 670

RESULT 224

XX AAK50428

XX ID AAK50428 standard; cDNA; 848 BP.

XX AAK50428;

XX 18-JUN-1999 (first entry)

XX Extended cDNA derived from 5' EST.

XX Human; secreted protein; EST; expressed sequence tag; diagnosis;

XX forensic; gene therapy; chromosome mapping; signal peptide; prostate;

XX upstream regulatory sequence; cytokine activity; cell proliferation;

XX differentiation; haematopoiesis regulation; tissue growth regulation;

XX reproductive hormone regulation; chemokine; chemokine; haemostatic;

XX thrombolytic; anti-inflammatory; tumour inhibition; ds.

XX Homo sapiens.

XX WO9906550-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WO-IB001232.

XX 01-AUG-1997; 97US-00905144.

XX (BEST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Lacroix B;

XX WPI; 1999-153780/13.

DR P-PSDB; AAY11715.

XX New isolated prostate-derived nucleic acids - used to develop products
PT which may have cytokine, immune regulatory, haemacopoiesis regulating,
XX anti-inflammatory or tumour inhibition activity.

PS Example 28; Page 160-161; 675bp; English.

XX AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins expressed in prostate, and encode the proteins
CC given in AAY11716 to AAY11993 respectively. The proteins given represent
CC the signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation and differentiation activity, haemacopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptides can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell
XX

SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 2; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181; Indels 1; Gaps 1;
Matches 634; Conservative 4; Mismatches 0;

QY 1 ATGTGTGGCTGCTCTTTTTCGTGTCAGTCGCAATTCAGTGAATCTGTCAACAGGT 60
DB 32 ATGTGTGGCTGCTCTTTTTCGTGTCAGTCGCAATTCAGTGAATCTGTCAACAGGT 91
QY 61 GCAGAAAATGCTTTTAAAGTAGACTGTATCAAGACAGCTCTGGAGATTAACATAT 120
DB 92 GCAGAAAATGCTTTTAAAGTAGACTGTATCAAGACAGCTCTGGAGATTAACATAT 151
QY 121 GCCTGGGATACCAATGAAGATACCTCTTCAAGGAGTGTGAGCTTCTCCATGAGAAA 180
DB 152 GCCTGGGATACCAATGAAGATACCTCTTCAAGGAGTGTGAGCTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAACAGAAATTTCCATGTCTTCTTGTGATGTAACCAAGG 240
DB 212 GTTCCCAACAGAGAACAGAAATTTCCATGTCTTCTTGTGATGTAACCAAGG 271
QY 241 GTATCATTCCTGTTGTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 300
DB 272 GTATCATTCCTGTTGTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 331
QY 301 GTGCAATACGCAATTAAGATGAAGAACCGGATCAACATGCTCTTCTTAATGAC 360
DB 332 GTGCAATACGCAATTAAGATGAAGAACCGGATCAACATGCTCTTCTTAATGAC 391
QY 361 CAATCTGGAATTTTAAATTCCTTCCACATTCGACCAACCAATGACCATCTGTG 420
DB 392 CAATCTGGAATTTTAAATTCCTTCCACATTCGACCAACCAATGACCATCTGTG 451
QY 421 CCCATCTGGAATTTTAAATTCCTTCCACATTCGACCAACCAATGACCATCTGTG 480
DB 452 CCCATCTGGAATTTTAAATTCCTTCCACATTCGACCAACCAATGACCATCTGTG 511
QY 481 CTGATTTTATCGAGGATCTGGCAGCTGAGAGAAAGAAACCAAGACCATCTGAATGAT 540
DB 512 CTGATTTTATCGAGGATCTGGCAGCTGAGAGAAAGAAACCAAGACCATCTGAATGAT 571
QY 541 GACGCTGAAGATTAAGTGTGAAAAACATGATCAATTTGAAATGGACATCCCTCTGATCC 600
DB 572 GACGCTGAAGATTAAGTGTGAAAAACATGATCAATTTGAAATGGACATCCCTCTGATCC 631
QY 601 CTGGAACATGAAGGG-GGGCATTTAATGATGCTTCATG 638

DB 632 CTGGAACATGAAGGGGCGCATTTAATGATGCTTCATG 670

RESULT 225

AAZ42251
ID AAZ42251 standard; cDNA; 848 BP.

XX AAZ42251;

XX 01-FEB-2000 (first entry)

XX Human full length cDNA 58-35-2-F10-Fl2.

XX Human, 5' EST, expressed sequence tag; secreted protein; diagnosis;
XX gene therapy; chromosome mapping; upstream regulatory sequence; forensic;
XX location; development; protein synthesis; stability; regulation;
XX identification; ss.

XX Homo sapiens.

XX WO953051-A2.

XX 21-OCT-1999.

XX 09-APR-1999; 99WO-IB000712.

XX 09-APR-1998; 98US-00057719.

XX 28-APR-1998; 98US-00069047.

XX (GBST) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-038446/03.

XX P-PSDB; AAY64646.

XX Novel secreted protein 5' expressed sequence tag sequences used in
XX diagnostic, forensic, gene therapy, and chromosome mapping procedures.

XX Example 21; Page 167-168; 837bp; English.

XX AAZ42265 to AAZ43075 represent novel 5' expressed sequence tag (EST)
XX sequences, corresponding to human secreted proteins. AAY64651 to AAY65438
XX represent the EST-related proteins corresponding to AAZ42265 to AAZ43075.
XX The 5' ESTs can be used for producing secreted human gene products. They
XX can be used to identify and isolate 5' untranslated regions (UTRs) and
XX upstream regulatory regions which control the location, development
XX stage, rate, and quantity of protein synthesis, as well as stability of
XX mRNA. The ESTs are also useful as probes for chromosome mapping, and to
XX obtain full length cDNA clones. The ESTs can also be used in forensic
XX procedures to identify individuals, or in diagnostic procedures to
XX identify individuals having genetic diseases resulting from abnormal gene
XX expression. The products may also be used in gene therapy protocols. The
XX nucleic acids encoding signal peptides can be used for directing
XX extracellular secretion of a polypeptide or the insertion of a cell. The
XX polypeptide into a membrane, or importing a polypeptide into a cell. The
XX proteins encoded by the EST sequences may be useful in treating a variety
XX of human conditions. Secreted proteins have therapeutic value, and the
XX identification of new secreted proteins is valuable. AAZ42249 to AAZ42264
XX and AAY64644 to AAY64650 represent sequences used in the exemplification
XX of the present invention

SQ Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;

Query Match 98.0%; Score 625; DB 3; Length 848;

Best Local Similarity 99.2%; Pred. No. 8.7e-181; Indels 1; Gaps 1;
Matches 634; Conservative 4; Mismatches 0;

QY 1 ATGTGTGGCTGCTCTTTTTCGTGTCAGTCGCAATTCAGTGAATCTGTCAACAGGT 60
DB 32 ATGTGTGGCTGCTCTTTTTCGTGTCAGTCGCAATTCAGTGAATCTGTCAACAGGT 91


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Db 512 CTGATTTTATCAGGATCTGGACAGCTADAAARAAAAGAACCATCTGAATGTGAT 571
Qy 541 GAGCGTGAAGATTAAGTGTGAACAAATGATCAATATTGAATGGATCCCTGATGCC 600
Db 572 GAGCGTGAAGATTAAGTGTGAACAAATGATCAATATTGAATGGATCCCTGATGCC 631
Qy 601 CTGACATGAAGGG-GGGCATTTTAAATGATGCTTCATG 638
Db 632 CTGACATGAAGGGGAGGAGCATATTAATGATGCTTCATG 670

RESULT 227
AAK8191
ID AAK8191 standard; cDNA, 848 BP.
XX
AC AAK8191;
XX
DT 23-SEP-1999 (first entry)
XX
DE Human secreted protein 6 extended cDNA.
XX
KM Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
KM diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 32..700
FT /tag= a
FT /product= "secreted protein"
XX
XX W09925825-A2.
XX
PD 27-MAY-1999.
XX
XX 13-NOV-1998; 98MO-IB001862.
XX
XX 13-NOV-1997; 97US-0066677P.
XX
PR 17-DEC-1997; 97US-0069957P.
XX
PR 09-FEB-1998; 98US-0074121P.
XX
PR 13-APR-1998; 98US-0081563P.
XX
PR 10-AUG-1998; 98US-0096116P.
XX
PR 04-SEP-1998; 98US-0099273P.
XX
XX
XX (GENSET ) GENSET.
XX
PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
XX
XX WPI; 1999-347472/29.
XX
DR P-PSDB; AAY25459, AAY25460.
XX
XX
XX Extended cDNAs encoding secreted proteins.
XX
XX
XX Example 28; Page 138; 307p; English.
XX
XX This invention describes novel nucleic acid sequences of extended cDNAs
XX (see AAK97813-X97906) which encode human secreted proteins (see AAY36129-
XX Y36222) and which have cytostatic, thrombotic and osteopathic activity.
XX The extended cDNAs can be used to express secreted proteins or parts of
XX them or to obtain antibodies capable of binding to the secreted proteins.
XX They may also be used in diagnostic, forensic, gene therapy and
XX chromosome mapping procedures. Uses also include design of expression
XX vectors and secretion vectors. This sequence represents an extended cDNA
XX sequence which encodes a secreted protein used in the method of the
XX invention
XX
XX
XX Sequence 848 BP; 257 A; 180 C; 161 G; 244 T; 0 U; 6 Other;
XX
XX
XX Query Match 97.9%; Score 624.4; DB 2; Length 848;
XX Best Local Similarity 99.2%; Pred. No. 1,3e-180;
XX Matches 634; Conservative 3; Mismatches 1; Indels 1; Gaps 1;
XX
XX 1 ATGTTGGCTGCTCTTTTCTGTGACATTCATGCTGAACCTGTCACCAAGGT 60
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```
Db 32 ATGTTGGCTGCTCTTTTCTGTGACATTCATGCTGAACCTGTCACCAAGGT 91
Qy 61 GCGAAGAAATGCTTTTAAAGTGAAGCTTAGTATCAGAACAGCTCTGGAGATTAAGCAT 120
Db 92 GCGAAGAAATGCTTTTAAAGTGAAGCTTAGTATCAGAACAGCTCTGGAGATTAAGCAT 151
Qy 121 GCTTGGAGATACCAATGAAGAAATACCTCTTCAAGAGAGATGACTTTCTTCATGAGAAA 180
Db 152 GCTTGGAGATACCAATGAAGAAATACCTCTTCAAGAGAGATGACTTTCTTCATGAGAAA 211
Qy 181 GTTCCCAACAGAGAGCAACAGAAATTTCCAGTGTCTTCTGCAATGTAACCCGAGG 240
Db 212 GTTCCCAACAGAGAGCAACAGAAATTTCCAGTGTCTTCTGCAATGTAACCCGAGG 271
Qy 241 GTATCATTTCTGTTGTGTTACAGACCTTCAGAAAATCAGACCTTCTCTGTTGAG 300
Db 272 GTATCATTTCTGTTGTGTTACAGACCTTCAGAAAATCAGACCTTCTCTGTTGAG 331
Qy 301 GTGCAATCAGCCATTAAGAAATGAACAGAACCCGATCAACATGCTTTCTTTAAATGAC 360
Db 332 GTGCAATCAGCCATTAAGAAATGAACAGAACCCGATCAACATGCTTTCTTTAAATGAC 391
Qy 361 CAACTCTGGAATTTTAAATCCCTTCCACACTTGCACCAACCAATGCAATCTGAG 420
Db 392 CAACTCTGGAATTTTAAATCCCTTCCACACTTGCACCAACCAATGCAATCTGAG 451
Qy 421 CCCATCTGATTAATTAATTTTGTGATTAATTTTGCATCATGATGTAATGCAATGCACTA 480
Db 452 CCCATCTGATTAATTAATTTTGTGATTAATTTTGCATCATGATGTAATGCAATGCACTA 511
Qy 481 CTGATTTTATCAGGAGATCTGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 512 CTGATTTTATCAGGAGATCTGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
Qy 541 GAGCGTGAAGATTAAGTGTGAACAAATGATCAATATTGAATGGATCCCTGATGCC 600
Db 572 GAGCGTGAAGATTAAGTGTGAACAAATGATCAATATTGAATGGATCCCTGATGCC 631
Qy 601 CTGACATGAAGGG-GGGCATTTTAAATGATGCTTCATG 638
Db 632 CTGACATGAAGGGGAGGAGCATATTAATGATGCTTCATG 670

RESULT 228
AAK30083
ID AAK30083 standard; cDNA, 847 BP.
XX
XX AAK30083;
XX
XX 17-JUN-1999 (first entry)
XX
XX
XX Human secreted protein 5' EST SEQ ID NO:27.
XX
XX
XX Human, secreted protein; EST; expressed sequence tag; diagnosis;
XX forensic; gene therapy; chromosome mapping; signal peptide;
XX upstream regulatory sequence; cytokine activity; cell proliferation;
XX differentiation; haematopoiesis regulation; tissue growth regulation;
XX reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
XX thrombolytic; anti-inflammatory; tumour inhibition; dr.
XX
XX
XX Homo sapiens.
XX
XX W09906548-A2.
XX
XX 11-FEB-1999.
XX
XX 31-JUL-1998; 98MO-IB001222.
XX
XX 01-AUG-1997; 97US-00905135.
XX
XX (GENSET ) GENSET.
XX
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PI Dumas Milne Edwards J, Duclert A, Lacroix B;
XX MPI, 1999-153778/13.
XX P-PSDB; AAY04174.

XX New nucleic acids encoding human secreted proteins - obtained from cDNA
PT libraries prepared from e.g. liver, brain, prostate, kidney, lung,
PT umbilical cord, placenta and colon tissue.

PS Example 28; Page 174-175; 824pp; English.

XX AAX41094 to AAX41347 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY12261 to
CC AAY12514, respectively. The proteins given represent the signal peptide
CC and an N-terminal fragment of a secreted protein. The nucleic acid
CC sequences can be used for producing secreted human gene products. They
CC can also be used to develop products for diagnosis and therapy. The
CC proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoietic regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide or the insertion of a
CC polypeptide into a membrane, or importing a polypeptide into a cell. The
CC present sequence represents a 5' EST from an example of the present
CC invention

SO Sequence 847 BP; 257 A; 178 C; 162 G; 244 T; 0 U; 6 Other;

Query Match 97.7%; Score 623.4; DB 2; Length 847;
Best Local Similarity 99.1%; Pred. No. 2,7e-180;
Matches 633; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

```
QY 1 AATGTTGCTGCTCTTTTCTGAGACGTCATTCATGCAACCTGCAACGAGT 60
DB |||
QY 32 ATGTTGCTGCTCTTTTCTGAGACGTCATTCATGCAACCTGCAACGAGT 91
DB |||
QY 61 GCAGAAATGCTTTTAAAGTAGACTAGTACGAACAGCTCTGGAGATTAAGCATAT 120
DB |||
QY 92 GCAGAAATGCTTTTAAAGTAGACTAGTACGAACAGCTCTGGAGATTAAGCATAT 151
DB |||
QY 121 GCTTGGATACCAATGAGATACCTTTCAAGCGATGAGCTTTCTCCATGAGAAA 180
DB |||
QY 152 GCTTGGATACCAATGAGATACCTTTCAAGCGATGAGCTTTCTCCATGAGAAA 211
DB |||
QY 181 GTTCCCAACAGAGACCAAGAAATTTCCCATGCTCTTTCATGATTAACCAAGG 240
DB |||
QY 212 GTTCCCAACAGAGACCAAGAAATTTCCCATGCTCTTTCATGATTAACCAAGG 271
DB |||
QY 241 GATCATCTGCTTTGTTGTTTACAGACCTTCAAAAATATCAACCTCTGCTGTTGAG 300
DB |||
QY 272 GATCATCTGCTTTGTTGTTTACAGACCTTCAAAAATATCAACCTCTGCTGTTGAG 331
DB |||
QY 301 GTGCAATCAGCCATTAAGATGAACAGAACCGATCAACATGCTTTCTTAATGAC 360
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QY 332 GTGCAATCAGCCATTAAGATGAACAGAACCGATCAACATGCTTTCTTAATGAC 391
DB |||
QY 361 CAAATCTGGAATTTTAAATCCCTTCAACCTTGCACACCAACCAAGCAATCTGAG 420
DB |||
QY 392 CAAATCTGGAATTTTAAATCCCTTCAACCTTGCACACCAACCAAGCAATCTGAG 451
DB |||
QY 421 CCATCTGATATTAATATTTGTTGATATTTTGCATCATCATAGTGGCAATGCACTA 480
DB |||
QY 452 GCATCTGATATTAATATTTGTTGATATTTTGCATCATCATAGTGGCAATGCACTA 511
DB |||
QY 481 CTGATTTTATCAGGAGATCTGGCAACGTAGAGAAAGAAACCAAGCAATCTGAGTGGAT 540
DB |||
QY 512 CTGATTTTATCAGGAGATCTGGCAACGTAGAGAAAGAAACCAAGCAATCTGAGTGGAT 571
DB |||
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QY 541 GACCTGAGATTAAGTGTGAAAAACATGATCAATTCAGAAATGSCATCCCTGATCCC 600
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QY 572 GACCTGAGATTAAGTGTGAAAAACATGATCAATTCAGAAATGSCATCCCTGATCCC 631
DB |||
QY 601 CTGACATGAAGG-GGGCATATTAATGATGCTTCATG 638
DB |||
QY 632 CTGACATGAAGGAGGAGGCAATTAATGATGCTTCATG 670
DB |||
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RESULT 229

AAH98224/c

ID AAH98224 standard; cDNA; 1365 BP.

AC AAH98224;

DT 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 81.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

XX gene therapy; nutrition; ss.

XX Homo sapiens.

XX WO200154477-A2.

XX 25-JAN-2001; 2001MO-US002687.

XX 25-JAN-2001; 2000US-00491404.

XX 17-JUL-2000; 2000US-00617746.

XX 03-AUG-2000; 2000US-00631451.

XX 15-SEP-2000; 2000US-00663870.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V,

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX MPI; 2001-476164/51.

XX P-PSDB; AAM23565.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use.

XX Claim 1; Page 234; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

XX proteins from a variety of organisms, including human, dog, cat, horse,

XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

XX urchin and tomato. These were derived from expressed sequence tags (ESTs)

XX from the organism of interest. They can be used in diagnostics,

XX forensics, gene mapping, identification of mutations, to assess

XX biodiversity and for nutritional purposes. The present sequence is a cDNA

XX of the invention

SO Sequence 1365 BP; 416 A; 244 C; 257 G; 448 T; 0 U; 0 Other;

Query Match 96.6%; Score 616; DB 4; Length 1365;
Best Local Similarity 99.7%; Pred. No. 6.2e-178;
Matches 638; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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DB |||
QY 1335 ATGTTGCTGCTCTTTTCTGAGACGTCATTCATGCAACCTGCAACGAGT 1276
DB |||
QY 61 GCAGAAATGCTTTTAAAGTAGACTAGTACGAACAGCTCTGGAGATTAAGCATAT 120
DB |||
QY 1275 GCAGAAATGCTTTTAAAGTAGACTAGTACGAACAGCTCTGGAGATTAAGCATAT 1216
DB |||
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XX 20-NOV-2003 (first entry)
 DT Human secreted protein encoding cDNA.
 XX
 XX
 XX Human, secreted protein; cancer; hyperproliferative disorder;
 XX rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
 XX anaemia; allergic reaction; asthma; cardiovascular disorder;
 XX wound healing; cytostatic; immunosuppressive; neuroprotective;
 XX antiviral; anti-allergic; hepatotropic; antidiabetic; anti-inflammatory;
 XX vulnerary; cardiant; gene therapy; ss.
 OS Homo sapiens.
 XX
 XX WO2002102993-A2.
 XX
 XX 27-DEC-2002.
 XX
 XX 19-MAR-2002; 2002MO-US008123.
 XX
 XX 21-MAR-2001; 2001US-0277340P.
 XX 19-JUL-2001; 2001US-0306171P.
 XX 13-NOV-2001; 2001US-0331287P.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Ruben SM;
 XX WPI; 2003-175238/17.
 XX
 XX New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.
 XX
 XX Claim 9; SEQ ID NO 763; 3205pp; English.
 XX
 XX The invention relates to novel genes ADA39629-ADA40565 and proteins
 CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
 CC treating or ameliorating medical conditions e.g. by protein or gene
 CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
 CC fragments, and agonists or antagonists that bind to the polypeptide are
 CC useful for preparing a diagnostic or pharmaceutical composition for
 CC diagnosing or treating cancer or other hyperproliferative disorder. The
 CC polypeptides and nucleic acid molecules are also useful for detecting,
 CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
 CC or other hyperproliferative disorders including neoplasms, autoimmune
 CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 CC thrombocytopenia), allergic reactions including asthma or eczema,
 CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 CC range restriction mapping, as molecular weight markers, or as
 CC hybridization or diagnostic probes. The polypeptides and antibodies are
 CC useful for providing immunological probes for differential identification
 CC of the tissues immunohistochemistry assays. Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/publicated_pct_sequences.
 XX
 XX Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;
 SO
 Query Match 96.4%; Score 615; DB 7; Length 1356;
 Best Local Similarity 99.7%; Pred. No. 1.3e-177;
 Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
 QY 1 ATGTGTGGCTGCTCTTTTCTGTGTACATCCATATCATGTGTAAGTCTGTCAACAGGT 60

Db 18 ATGTGTGGCTGCTCTTTTCTGTGTACATCCATATCATGTGTAAGTCTGTCAACAGGT 77
 QY 61 GCAGAAAATGCTTTTAAAGTACCTTATCTGAAACAGCTCTGGGATTAAGCATAT 120
 Db 78 GCAGAAAATGCTTTTAAAGTACCTTATCTGAAACAGCTCTGGGATTAAGCATAT 137
 QY 121 GCGCGGATTCAGTAAAGAAATACCTCTTCAAGCATAGTACTTCTCCATGAGAAA 180
 Db 138 GCGCGGATTCAGTAAAGAAATACCTCTTCAAGCATAGTACTTCTCCATGAGAAA 197
 QY 181 GTTCCCAACAGAGAGACAGAAATTCCTCATCTTGTGATTAATGAC 240
 Db 198 GTTCCCAACAGAGAGAGACAGAAATTCCTCATCTTGTGATTAATGAC 256
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 Db 257 GTATCATCTGTGTGTGTGTATCAAGCCCTTCAAAAATTCACACCTTCTGCTGTAG 316
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 Db 317 GTGCAATCAGCCATTAAGATGAAGACAGAGAGGATCAATGCTCTTCAATGAC 376
 QY 361 CAAACTCTGAATTTTAAATTCCTTCAACACTTGACACCAATGACCTCTGTG 420
 Db 377 CAAACTCTGAATTTTAAATTCCTTCAACACTTGACACCAATGACCTCTGTG 436
 QY 421 CCATCTGATTAATTAATTTGTGTGATATTTTGCATCATATGTTGCAATGACAT 480
 Db 437 CCATCTGATTAATTAATTTGTGTGATATTTTGCATCATATGTTGCAATGACAT 496
 QY 481 CTGATTTTATGAGGATCTGCAACGTGAAGAAAGACAAAGACATCTGAATGAT 540
 Db 497 CTGATTTTATGAGGATCTGCAACGTGAAGAAAGACAAAGACATCTGAATGAT 556
 QY 541 GACGCTGAAGATTAAGTGAAGAAACATGATCAATTTGAATGCAATCCCTGATCC 600
 Db 557 GACGCTGAAGATTAAGTGAAGAAACATGATCAATTTGAATGCAATCCCTGATCC 616
 QY 601 CTGACATGAAGAG-GGCGATATTAATGATGCTTATG 638
 Db 617 CTGACATGAAGAGAGGCGATATTAATGATGCTTATG 655
 RESULT 233
 AD411594
 ID AD411594 standard; DNA; 1356 BP.
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 XX AC AD411594;
 DT 06-NOV-2003 (first entry)
 XX
 XX Human cDNA encoding a novel secreted protein, SEQ ID NO 122.
 XX
 XX cancer; inflammation; immune disorder; neurological disorder;
 XX blood clotting disorder; food additive; food preservative;
 XX storage capability; fat content; nutritional component; ds; gene: human.
 XX
 XX Homo sapiens.
 XX
 XX US2003055236-A1.
 XX
 XX 20-MAR-2003.
 XX
 XX 14-MAR-2002; 2002US-00097065.
 XX
 XX 18-DEC-1997; 97US-0068006P.
 XX 18-DEC-1997; 97US-0068007P.
 XX 18-DEC-1997; 97US-0068008P.
 XX 18-DEC-1997; 97US-0068003P.
 XX 18-DEC-1997; 97US-0068004P.
 XX 18-DEC-1997; 97US-0068005P.
 XX 18-DEC-1997; 97US-0068006P.

CC identification, radiation hybrid mapping or long-range restriction
CC mapping, as molecular weight markers, or as hybridization or diagnostic
CC probes. The polypeptides and antibodies are useful for providing
CC immunological probes for differential identification of the tissues
CC immunohistochemistry assays. The present sequence represents a human
CC secreted protein encoding sequence.

XX Sequence 1356 BP; 460 A; 252 C; 240 G; 403 T; 0 U; 1 Other;

Query Match 96.4%; Score 615; DB 9; Length 1356;

Best Local Similarity 99.7%; Pred. No. 1.3e-177;

Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1 ATGTGTGCTGCTCTTTTCTGTGTGACCTGCAATTCAGTGAACCTGTGCAACAGGT 60
   |||||
Db 18 ATGTGTGCTGCTCTTTTCTGTGTGACCTGCAATTCAGTGAACCTGTGCAACAGGT 77
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QY 61 GCAGAAAATGCTTTAAAGTGAGACTTGTATCAGAACAGCTCTGGAGATAAGCATAT 120
   |||||
Db 78 GCAGAAAATGCTTTAAAGTGAGACTTGTATCAGAACAGCTCTGGAGATAAGCATAT 137
   |||||

QY 121 GCCTGGATACCAATGAAGAATACCTCTCAAGGAGATGTAGCTTCTCCATGAGAAA 180
   |||||
Db 138 GCCTGGATACCAATGAAGAATACCTCTCAAGGAGATGTAGCTTCTCCATGAGAAA 197
   |||||

QY 181 GTTCCCAACAGAGAACACAGAAATTTCCATGTCTACTTGCATGTAAACCAAGG 240
   |||||
Db 198 GTTCCCAACAGAGAACACAGAAATTTCCATGTCTACTTGCATGTAAACCAAGG 256
   |||||

QY 241 GTATCATTTCTGTTGTGTGTACAGACCTTCAAAAATCACAACCTTCTGCTGTGAG 300
   |||||
Db 257 GTATCATTTCTGTTGTGTGTACAGACCTTCAAAAATCACAACCTTCTGCTGTGAG 316
   |||||

QY 301 GTGCAATCAGCCATTAAGATGAACAAGAACGGATCAACATGCTTCTTTCTAAATGAC 360
   |||||
Db 317 GTGCAATCAGCCATTAAGATGAACAAGAACGGATCAACATGCTTCTTTCTAAATGAC 376
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QY 361 CAAACTCTGAAATTTTAAAAATCCCTTCACACTTGCACCAACCAATGACCTGTG 420
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Db 377 CAAACTCTGAAATTTTAAAAATCCCTTCACACTTGCACCAACCAATGACCTGTG 436
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QY 421 CCCATCTGATTTATTAATTTGTGTGTATTTTGCATGATGATGCAATGCAATGCACTA 480
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Db 437 CCCATCTGATTTATTAATTTGTGTGTATTTTGCATGATGATGCAATGCAATGCACTA 496
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QY 481 CTGATTTTATCAGGAGATCTGGCAAGTGAAGAAACAAAGAACATCTGAAGTGAT 540
   |||||
Db 497 CTGATTTTATCAGGAGATCTGGCAAGTGAAGAAACAAAGAACATCTGAAGTGAT 556
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QY 541 GACGCTGAAGATTAAGTGAACATGATCACAATGAAATGCAATCCCTGTGATCC 600
   |||||
Db 557 GACGCTGAAGATTAAGTGAACATGATCACAATGAAATGCAATCCCTGTGATCC 616
   |||||

QY 601 CTGACATGAAGAGG-GGGCATTTTAATGATGCTTCATG 638
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Db 617 CTGACATGAAGAGGAGGCATTTTAATGATGCTTCATG 655
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Search completed: June 6, 2004, 10:56:53
Job time : 283.223 secs

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Db 67 GCAGAAATGCTTTTAAAGTGAAGTATGATGAGAAAGCTCTGGAGATTAAGCATAT 126
Qy 121 GCTGGGATACCAATTAAGATACCTCTCAAGGATGTAGCTTTCCCATGAGAAA 180
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Qy 241 GATCATCTGTGTGTGTGTACAGACCTTCAAAAATCAACACCTTCTGTGTAG 300
Db 247 GATCATCTGTGTGTGTGTACAGACCTTCAAAAATCAACACCTTCTGTGTAG 306
Qy 301 GTGCAATCGCCATTAAGATTAAGAAACCAAGAACCGGATCAACATGCTTTCTAAATGAC 360
Db 307 GTGCAATCGCCATTAAGATTAAGAAACCAAGAACCGGATCAACATGCTTTCTAAATGAC 366
Qy 361 CAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGACCCATCTGTG 420
Db 367 CAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGACCCATCTGTG 426
Qy 421 CCATCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGACCCATCTGTG 480
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Db 547 GACGCTGAAGATTAAGTGTGTAACCATGATCACAATGAAATGGCATCCCTCTGATCCC 606
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RESULT 2
AX403499 1346 bp DNA linear PAT 14-JUN-2002
LOCUS AX403499
DEFINITION Sequence 386 from Patent WO0073454.
ACCESSION AX403499
VERSION AX403499.1 GI:21436987
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D.,
Farrar, N., Gerber, H., Gertsen, M., Goddard, A., Godowski, P.,
Grimaldi, C.J., Gurney, A.L., Kijavich, I., Napier, M.A., Pan, J.,
Paoni, N.P., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Williams, P., Wood, M.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0073454-A 386 07-DEC-2000;
JOURNAL Genentech Inc. (US)
FEATURES
source 1. 1346
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 638; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.4e-165;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGTGCTGCTCTTTTCTGTGACTGCATTCATGCTGAACCTCTGTCAACAGGT 60

|||||
Db 7 ATGTGTGCTGCTCTTTTCTGTGACTGCATTCATGCTGAACCTCTGTCAACAGGT 66
Qy 61 GCAGAAATGCTTTTAAAGTGAAGTATGATGAGAAAGCTCTGGAGATTAAGCATAT 120
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Qy 121 GCTGGGATACCAATTAAGATACCTCTCAAGGATGTAGCTTTCCCATGAGAAA 180
Db 127 GCTGGGATACCAATTAAGATACCTCTCAAGGATGTAGCTTTCCCATGAGAAA 186
Qy 181 GTTCCCAACAGAGAACCAAGAAATTTCCCATGTCTCACTTTCATATGAACCCAGAG 240
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Db 427 CCATCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGACCCATCTGTG 486
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Db 487 CTGATTTTACAGGATCTGGCAACCTTAAGAAAGAAACCAAGAACCATCTGAATGACAT 546
Qy 541 GACGCTGAAGATTAAGTGTGTAACCATGATCACAATGAAATGGCATCCCTCTGATCCC 600
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Qy 601 CTGACATGAGAGGGGGCATATTATGATGCTTCATG 638
Db 607 CTGACATGAGAGGGGGCATATTATGATGCTTCATG 644

RESULT 3
AX464348 1346 bp DNA linear PAT 16-JUL-2002
LOCUS AX464348
DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Baker, K.P., Beresini, M., Deforge, L., Desnovers, L., Flyvbjerg, B.,
Gao, W.O., Gertsen, M.B., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, M.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0140466-A 481 07-JUN-2001;
JOURNAL Genentech Inc. (US)
FEATURES
source 1. 1346
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 100.0%; Score 638; DB 6; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.4e-165;
Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGTGTGCTGCTCTTTTCTGTGACTGCATTCATGCTGAACCTCTGTCAACAGGT 60

Matches	638; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
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Qy	61	GCAGAAAATGCTTTTAAAGTGAAGTCTTACTATCAGAACGCTCTGGAGATTAAGCAT	120		
Db	67	GCAGAAAATGCTTTTAAAGTGAAGTCTTACTATCAGAACGCTCTGGAGATTAAGCAT	126		
Qy	121	GCTGGGGATACCAATGAAGAAATACCTCTTCAAGAGATGCTGCTTCTCCATGAGAAA	180		
Db	127	GCTGGGGATACCAATGAAGAAATACCTCTTCAAGAGATGCTGCTTCTCCATGAGAAA	186		
Qy	181	GTTCCCAACAGAGAACAGAAATTTCCATGTCCTACTTTCGATGTAACCCAGAG	240		
Db	187	GTTCCCAACAGAGAACAGAAATTTCCATGTCCTACTTTCGATGTAACCCAGAG	246		
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Db	367	CAAACTCTGGAATTTTAAAAATCCCTTCCACATTCGACCAACCCATGACCTGTG	426		
Qy	421	CCCATCTGGATTAATTAATTTGGTGAATTTTTCATTCATGATGATGCAATTCACAT	480		
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Db	487	CTGATTTTATCAGAGATTTGCGCAAGTGAAGAAACAAAGAACCATCTGAAGTGA	546		
Qy	541	GACCTGGAATGAATGATGTAAGAAACATGATCAATTTGAAGATGCAATCCCTGTATCC	600		
Db	547	GACCTGGAATGAATGATGTAAGAAACATGATCAATTTGAAGATGCAATCCCTGTATCC	606		
Qy	601	CTGACATGAAGGGGGGCATTAATTAATGATGCTTCATG	638		
Db	607	CTGACATGAAGGGGGGCATTAATTAATGATGCTTCATG	644		
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LOCUS	AY359060	1346 bp	mRNA	linear	PRI 03-OCT-2003
DEFINITION	Homo sapiens clone DNA61873 NX-17 (UNQ678)	mRNA, complete cds.			
ACCESSION	AY359060	1	GI:37183237		
VERSION	AY359060.1	GI:37183237			
KEYWORDS	PII_CDNA.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1346)				
	Clark,H.F., Gurney,A.L., Abaya,B., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Delen,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Haas,P.B., Heldens,S., Huang,A., Kim,H.S., Klimewski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,B., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simons,L., Singh,J., Smith,V., Stinson,J., Vagstad,A., Vandlen,R., Watanabe,C., Weiland,D., Woods,K., Xie,M.H., Yamaura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.				
TITLE	The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment				
JOURNAL	Genome Res. 13 (10), 2265-2270 (2003)				
PUBMED	12975309				

REFERENCE	2 (bases 1 to 1346)				
AUTHORS	Clark,H.F.				
TITLE	Direct Submission				
JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA				
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ORIGIN					
Query Match	100.0%; Score 638; DB 9; Length 1346;				
Best Local Similarity	100.0%; Pred. No. 2.4e-165;				
Matches	638; Conservative	0; Mismatches	0; Indels	0; Gaps	0;
Qy	1	ANGTGTGGCTGCTCTCTTTTCTGAGTGCATTCATGCTGAATCTGTCAACAGGT	60		
Db	7	ATGTTGTGGCTGCTCTCTTTTCTGAGTGCATTCATGCTGAATCTGTCAACAGGT	66		
Qy	61	GCAGAAAATGCTTTTAAAGTGAAGTCTTACTATCAGAACGCTCTGGAGATTAAGCAT	120		
Db	67	GCAGAAAATGCTTTTAAAGTGAAGTCTTACTATCAGAACGCTCTGGAGATTAAGCAT	126		
Qy	121	GCTGGGGATACCAATGAAGAAATACCTCTTCAAGAGATGCTGCTTCTCCATGAGAAA	180		
Db	127	GCTGGGGATACCAATGAAGAAATACCTCTTCAAGAGATGCTGCTTCTCCATGAGAAA	186		
Qy	181	GTTCCCAACAGAGAACAGAAATTTCCATGTCCTACTTTCGATGTAACCCAGAG	240		
Db	187	GTTCCCAACAGAGAACAGAAATTTCCATGTCCTACTTTCGATGTAACCCAGAG	246		
Qy	241	GTAATCATCTGGTTTGTGGTTACAGACCTTCAAAAATACACACCTTCTGCTGTGAG	300		
Db	247	GTAATCATCTGGTTTGTGGTTACAGACCTTCAAAAATACACACCTTCTGCTGTGAG	306		
Qy	301	GTGCAATAGCAATGAAGATGAACAAAGACCGATCAACATGCTTCTTCTTAATGAC	360		
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Qy	361	CAAACTCTGGAATTTTAAAAATCCCTTCCACATTCGACCAACCCATGACCTGTG	420		
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Qy	481	CTGATTTTATCAGAGATTTGCGCAAGTGAAGAAACAAAGAACCATCTGAAGTGA	540		
Db	487	CTGATTTTATCAGAGATTTGCGCAAGTGAAGAAACAAAGAACCATCTGAAGTGA	546		
Qy	541	GACCTGGAATGAATGATGTAAGAAACATGATCAATTTGAAGATGCAATCCCTGTATCC	600		
Db	547	GACCTGGAATGAATGATGTAAGAAACATGATCAATTTGAAGATGCAATCCCTGTATCC	606		
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LOCUS	AX083392	1347 bp	DNA	linear	PAT 28-FEB-2001
SEQUENCE	84 from Patent WO0112660.				
ACCESSION	AX083392				
VERSION	AX083392.1	GI:13185232			
KEYWORDS					
ORGANISM	Homo sapiens (human)				
SOURCE	Homio sapiens Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 Kato, S. and Kimura, T. Human proteins having hydrophobic domains and dnase encoding these proteins Patent: WO 0112660-A 84 22-FEB-2001; SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)				
JOURNAL					
FEATURES					
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CDS					
Query Match	98.3%; Score 627; DB 6; Length 1347;				
Best Local Similarity	99.8%; Pred. No. 2,66-162;				
Matches 638; Conservative	0; Mismatches 0; Indels 1; Gaps 1;				
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Qy	26 ATGTTGGGCTGCTCTTTTTCGTGAGTCGCCATTCATGCTGACACTGTGCAACCAAGT 85				
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Qy	146 GCGTGGGATACCAATGAAGAATACCTCTTCAAGACGATGTAAGCTTCTCCATGAGAAA 205				
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Qy	266 GTATCATTTCTGTTGGTTAGTGAAGCCCTTCAAAAATATCAACCCCTTCTGCTGTGAG 325				
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Db	361 CAAATCTCGAAATTTTAAAAATCCCTTCCACATGTCACACCCAGGACCAATCTGTG 420				
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QY 481 CTGATTTATCAGGATCTGGCAAGTAGAAGAAAGAACCAATCTGAAGTGGAT 540
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Db 626 CTGACATGAAGGGAGGAGGATTAATGATGCTTCATG 664

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LOCUS BC050606 1377 bp mRNA linear PRI 12-NOV-2003
DEFINITION Homo sapiens kidney-specific membrane protein, mRNA (cDNA clone
MGC:60059 IMAGE:5183554), complete cds.
ACCESSION BC050606
VERSION BC050606.1 GI:30047080
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (base 1 to 1377)
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Strasberg, R.L., Feingold, R.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.P., Bat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Spletton, M., Soares, M.B., Bonaldo, M.P., Cabavant, T.L.,
Schaefer, T.E., Brownstein, M.J., Udell, T.B., Toehiyuki, S.,
Carninci, P., Prange, C., Kana, S.S., Lequellano, N.A., Peters, G.J.,
Armanaci, R.D., Mullahy, S.J., Bosak, S.A., McMan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Vallion, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Sanchez, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smillius, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
2388257
12477932
2 (bases 1 to 1377)
Strasberg, R.
Direct Submission
Submitted (08-APR-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcdbpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R.
M.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>
Series: IRAP Plate: 110 Row: C Column: 4
This clone was selected for full length sequencing because it

FEATURES
source passed the following selection criteria: matched mRNA gi: 21361864.
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Query Match 98.3%; Score 627; DB 9; Length 1377;
Best Local Similarity 99.8%; Pred. No. 2.6e-162;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 ANGTGTGCTGCTCTCTTTTTCGAGACTGCAATTCAGTGAAGTCTGCAACCAAGT 60
Db 9 ATGTTGTGCTGCTCTCTTTTTCGAGACTGCAATTCAGTGAAGTCTGCAACCAAGT 68
QY 61 GCAGAAATGCTTTTAAAGTAGACTTATGATCAGAACGCTTGGAGATTAAGCATAT 120
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QY 121 GCTTGGGATTCAGAAAGAAATACCTCTTCAAGGATGCTTCTTCATGAGAAA 180
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Db 249 GTATCATCTGTGTTGTGTTACAGACCTTCAAAAATCAGACCTTCTGCTGTGAG 308
QY 301 GTGCATACGCTTAAGAAATGAACAGAAACCGGATCAAAAGCTTCTTCAATAGAC 360
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Db 369 CAAACTGGAATTTTAAATAATCCCTTCCAGACTGACACCCATGAGACCATCTGTG 428
QY 421 CCCATCTGATTAATTAATTTGTTGTGATTAATTTTGCATCATCATAGTGCATGACAT 480
Db 429 CCCATCTGATTAATTAATTTGTTGTGATTAATTTTGCATCATCATAGTGCATGACAT 488
QY 481 CTGATTTTATCAGGATCTGGCAAGTAGAAGAAAGAACCAATCTGAAGTGGAT 540
Db 489 CTGATTTTATCAGGATCTGGCAAGTAGAAGAAAGAACCAATCTGAAGTGGAT 548
QY 541 GACGCTGAAGATAGTGTGAAGACATGATCAATTTGAAATGGCATCCCTTGATCCC 600
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QY 601 CTGACATGAAGGG-GGGCATTTTAATGATGCTTCATG 638

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1605)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marins, K., Parker, A.A., Rubin, G.M., Hong, L., Schect, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Stern, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Scherch, A., Schein, J.E., Jones, S.J., and Marra, M.A.
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE 22388257
 JOURNAL 12477932
 PUBLISHED 2 (bases 1 to 1605)
 REFERENCE Strausberg, R.
 AUTHORS Direct Submission
 JOURNAL Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILMIL)
 DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbiology.org>
 contact: amadan@systemsbiology.org
 Anup Madan, Jessica Fahy, Erin Helton, Mark Kesteman, Anuradha Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

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ORIGIN
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Query Match 98.3%; Score 627; DB 9; Length 1605;
 Best Local Similarity 99.8%; Pred. No. 2.6e-162;
 Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

1 AAGTTGGGCGGCTCTTTTCTGAGTCGTCATTCAGTGAAGTCAACAGGT 60
 261 AAGTTGGGCTGCTCTTTTCTGAGTCGTCATTCAGTGAAGTCAACAGGT 320
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 DEFINITION BD205644
 ACCESSION BD205644.1 GI:33015414
 VERSION JP 2002533058-A/21.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
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 1 (bases 1 to 1447)
 Ruben, S.M., Florence, K., Ni, J., Rosen, C.A., Carter, K.C., Moore, P.A., Olsen, H.S., Shi, Y., Young, P.B., Wei, F.F., Brewer, L.A., Soppet, D.R., Lafleur, D.W., Endress, G.A. and Ebner, R.R.
 97 human secreted proteins
 Patent: JP 2002533058-A 21 08-OCT-2002;
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 OS Homo sapiens (human)
 PN JP 2002533058-A/21

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		18-MAY-1998 US 60/085924, 18-MAY-1998 US 60/085922 PR	
		18-MAY-1998 US 60/085923, 18-MAY-1998 US 60/085921 PR	
		18-MAY-1998 US 60/085925, 18-MAY-1998 US 60/085928 PR	
	PI	STEVEN M RUBEN, KIMBERLY FLORENCE, JIAN NI, CRAIG A ROSEN, KENNETH	
	PI	C CARTER,	
	PI	PAUL A MOORE, HENRIK S OLSEN, YANGSU SHI, PAUL B YOUNG, PING FBI	
	PI	WEI,	
	PI	LAURIE A BREWER, DANIEL R SOPPET, DAVID W LAFLBUR, GREGORY A PI	
	ENDRES,		
	PI	REINHARD EBNER	
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DB	197	GCTTGGAATCCATGAAGAATCTCTTCAAAGCATGTAGCTTCTCCATGAGAAA	256
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ACCESSION	AF229179		
VERSION	AF229179.1 GI:9957753		
KEYWORDS			
SOURCE			
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	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
REFERENCE	1 (bases 1 to 1345)		
AUTHORS	Zhang,H., Wada,J., Hida,K., Tsuchiyaama,Y., Higashishi,K., Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.		
TITLE	Collectrin, a collecting duct-specific transmembrane glycoprotein, is a novel homolog of ACE2 and is developmentally regulated in embryonic kidneys		
JOURNAL	J Biol. Chem. 276 (20), 17132-17139 (2001)		
MEDLINE	21264468		
PUBMED	11278314		
REFERENCE	2 (bases 1 to 1345)		
AUTHORS	Zhang,H., Wada,J. and Makino,H.		
TITLE	Human kidney specific membrane protein (NX-17) Unpublished		
JOURNAL	3 (bases 1 to 1345)		
REFERENCE	Zhang,H., Wada,J. and Makino,H.		
AUTHORS	Submitted (28-JUN-2000) Department of Medicine III, Okayama University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558, Japan		
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	/protein_id="PAG09466.1"		
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	/translation="MTMLFLFPLVTAIHAEICOPGENAFVRVLSTIRLADKAYAMDTE NEELTFEAWVAFSGRKVBNBAKEISHLVLCNVTQVSFPVVTPDSEKHNTLPVEVO SAIKRNQRITNNAPRLNDOTLRPLKIPSTLAPEMDSPVIWIIIFGVYPCIIIVAILAL LTIISIQRRKKRPBSEBVDAEDCKENMITIENGIPSFDLMKGHINDAPFTBEDER LTPL"		
ORIGIN			
Query Match	98.0%; Score 625.4; DB 9; Length 1345;		
Best Local Similarity	99.7%; Pred. No. 7.2e-162;		
Matches 637; Conservative	0; Mismatches 1; Indels 1; Gaps 1;		
Oy	1	ATGTGTGGCTGCTCTTTTTCGTGAGACTGCCATTCATGCTGAACCTCTGTCAACAGGT	60
Db	24	ATGTGTGGCTGCTCTTTTTCGTGAGACTGCCATTCATGCTGAACCTCTGTCAACAGGT	83
Oy	61	GCAGAAAATGCTTTAAAGTGAGACTTAGTATCAAACAGCTCTGGAGATTAAGCATAT	120
Db	84	GCAGAAAATGCTTTAAAGTGAGACTTAGTATCAAACAGCTCTGGAGATTAAGCATAT	143
Oy	121	GCCCTGGATGCCAATGAAGAATACCTCTTCAAAAGCAATGGTAGCTTTCTCATAGAGAA	180
Db	144	GCCCTGGATGCCAATGAAGAATACCTCTTCAAAAGCAATGGTAGCTTTCTCATAGAGAA	203

QY 181 GTTCCCAAGAGAGCAAGAAATTTCCCATGCTTAATTGGCAATGTAACCGAGAG 240
DB 204 GTTCCCAAGAGAGCAAGAAATTTCCCATGCTTAATTGGCAATGTAACCGAGAG 263
QY 241 GTATCATTTCTGTTTGTGTGATACAGACCTTCAAAAAATCAACCTTCTGCTTTGAG 300
DB 264 GTATCATTTCTGTTTGTGTGATACAGACCTTCAAAAAATCAACCTTCTGCTTTGAG 323
QY 301 GTGCATCAGCCATTAAGATGAAGCAAGAACCGATCAACATGCTTCTTCTTAATGAC 360
DB 324 GTGCATCAGCCATTAAGATGAAGCAAGAACCGATCAACATGCTTCTTCTTAATGAC 383
QY 361 CAAACTCTGGAATTTTAAAAATCCCTTCAACATTTGACACCCATGAGACCCATCTG 420
DB 384 CAAACTCTGGAATTTTAAAAATCCCTTCAACATTTGACACCCATGAGACCCATCTG 443
QY 421 CCCATCTGGATTTATATATTTGGTGTGATTTTTCATCATATAGTTGCAATGCACTA 480
DB 444 CCCATCTGGATTTATATATTTGGTGTGATTTTTCATCATATAGTTGCAATGCACTA 503
QY 481 CTGATTTTATCAGGGATCTGGCACTGAGAAAGAAACAAAGAACCATGGAAGTGAAT 540
DB 504 CTGATTTTATCAGGGATCTGGCACTGAGAAAGAAACAAAGAACCATGGAAGTGAAT 563
QY 541 GACGCTGAAGATTAAGTGTGAAAAACATGATCACAATTTGAAATGSCATCCCTGTGATCC 600
DB 564 GACGCTGAAGATTAAGTGTGAAAAACATGATCACAATTTGAAATGSCATCCCTGTGATCC 623
QY 601 CTGACATGAAGG-GGGCATTTATATATGATGCTTCATG 638
DB 624 CTGACATGAAGGAGGGCATATATATGATGCTTCATG 662

RESULT 12
LOCUS BD083420 1401 bp DNA linear PAT 27-AUG-2002
DEFINITION Secreted proteins and polynucleotides encoding them.
ACCESSION BD083420
VERSION BD083420.1 GI:22629030
KEYWORDS JP 2001523950-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1401)
AUTHORS Jacobs, K., McCoy, J.M., Lavallic, E.R., Racie, L.A., Merberg, D.,
Tracy, M., Spaulding, V. and Agostino, M.J.
TITLE Secreted proteins and polynucleotides encoding them
JOURNAL Patent: JP 2001523950-A 2 27-NOV-2001;
GENETICS INSTITUTE INC
PN JP 2001523950-A/2
PD 27-NOV-2001
PF 23-JUN-1998 JP 1998532177
PR 24-JAN-1997 US 08/788789
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
DAVID MERBERG,
PI MAURICE TRACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC
CI2N15/12.CI2N5/10.C07K14/47.CI2Q/68.A6IK8/17 CC Strandedness:
Double;
CC Topology: linear;
FH Key Location/Qualifiers.
FEATURES
source 1..1401 Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 98.0%; Score 625.4; DB 6; Length 1401;
Best Local Similarity 99.7%; Pred. No. 7.2e-162;
Matches 637; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 1 ATGTTGTGGCTGCTCTTTTCTGTGAGCTGCATTCATGCTGAACCTGTGCAACCAAGT 60

DB 71 ATGTTGTGGCTGCTCTTTTCTGTGAGCTGCATTCATGCTGAACCTGTGCAACCAAGT 130
QY 61 GCAGAAAATGCTTTTAAAGTGAAGCTTAGTATCAGAACAGCTGTGGAGATTAAGCATAT 120
DB 131 GCAGAAAATGCTTTTAAAGTGAAGCTTAGTATCAGAACAGCTGTGGAGATTAAGCATAT 190
QY 121 GCTGGATACCAATGAAGAAATACCTTCAAGGAGTGAAGCTTCTTCATGAGAAA 180
DB 191 GCTGGATACCAATGAAGAAATACCTTCAAGGAGTGAAGCTTCTTCATGAGAAA 250
QY 181 GTTCCCAAGAGAGCAAGAAATTTCCCATGCTTAATTGGCAATGTAACCGAGAG 240
DB 251 GTTCCCAAGAGAGCAAGAAATTTCCCATGCTTAATTGGCAATGTAACCGAGAG 310
QY 241 GTATCATTTCTGTTTGTGTGATACAGACCTTCAAAAAATCAACCTTCTGCTTTGAG 300
DB 311 GTATCATTTCTGTTTGTGTGATACAGACCTTCAAAAAATCAACCTTCTGCTTTGAG 370
QY 301 GTGCATCAGCCATTAAGATGAAGCAAGAACCGATCAACATGCTTCTTCTTAATGAC 360
DB 371 GTGCATCAGCCATTAAGATGAAGCAAGAACCGATCAACATGCTTCTTCTTAATGAC 430
QY 361 CAAACTCTGGAATTTTAAAAATCCCTTCAACATTTGACACCCATGAGACCCATCTG 420
DB 431 CAAACTCTGGAATTTTAAAAATCCCTTCAACATTTGACACCCATGAGACCCATCTG 490
QY 421 CCCATCTGGATTTATATATTTGGTGTGATTTTTCATCATATAGTTGCAATGCACTA 480
DB 491 CCCATCTGGATTTATATATTTGGTGTGATTTTTCATCATATAGTTGCAATGCACTA 550
QY 481 CTGATTTTATCAGGGATCTGGCACTGAGAAAGAAACAAAGAACCATGGAAGTGAAT 540
DB 551 CTGATTTTATCAGGGATCTGGCACTGAGAAAGAAACAAAGAACCATGGAAGTGAAT 610
QY 541 GACGCTGAAGATTAAGTGTGAAAAACATGATCACAATTTGAAATGSCATCCCTGTGATCC 600
DB 611 GACGCTGAAGATTAAGTGTGAAAAACATGATCACAATTTGAAATGSCATCCCTGTGATCC 670
QY 601 CTGACATGAAGG-GGGCATTTATATATGATGCTTCATG 638
DB 671 CTGACATGAAGGAGGGCATATATATGATGCTTCATG 709

RESULT 13
LOCUS AR177334 848 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 27 from patent US 6312922.
ACCESSION AR177334
VERSION AR177334.1 GI:17919689
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards, J.-B., Dumas, Mline., Duclet, A. and Bouguetel, L.
TITLE Complementary DNAs
JOURNAL Patent: US 6312922-A 27 06-NOV-2001;
FEATURES
source 1..848 Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGTTGTGGCTGCTCTTTTCTGTGAGCTGCATTCATGCTGAACCTGTGCAACCAAGT 60
DB 32 ATGTTGTGGCTGCTCTTTTCTGTGAGCTGCATTCATGCTGAACCTGTGCAACCAAGT 91
QY 61 GCAGAAAATGCTTTTAAAGTGAAGCTTAGTATCAGAACAGCTGTGGAGATTAAGCATAT 120

Db 92 GAGAAATGCTTTAAAGTAGAGCTTAGATCAAGAACGCTCTGGAGATTAAAGCATAT 151
Qy 121 GCCTGGATACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 180
Db 132 GCTTGGATACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 211
Qy 181 GTTCCCAAGAGAGCAACAGAAATTTCCCATGTCCTTCACTTTGCAATGTAAACCGAGG 240
Db 212 GTTCCCAAGAGAGCAACAGAAATTTCCCATGTCCTTCACTTTGCAATGTAAACCGAGG 271
Qy 241 GATATCTTGTGTTTGTGTTTACAGACCTTCAAAAATCAACCCCTTCTGTGTAG 300
Db 272 GATATCTTGTGTTTGTGTTTACAGACCTTCAAAAATCAACCCCTTCTGTGTAG 331
Qy 301 GGCATACGACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 360
Db 332 GTGCAATACGACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 391
Qy 361 CAACTCTGGAATTTTAAATATCCCTTCACACTTGCACACCCATGACCCATCTGTG 420
Db 392 CAACTCTGGAATTTTAAATATCCCTTCACACTTGCACACCCATGACCCATCTGTG 451
Qy 421 CCCATCTGATTTATATATTTGGTGTGATTTTGTGATCATCATAGTGAATTGACAT 480
Db 452 CCCATCTGATTTATATATTTGGTGTGATTTTGTGATCATCATAGTGAATTGACAT 511
Qy 481 CTGATTTTATCAGGAGCTGCGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 512 CTGATTTTATCAGGAGCTGCGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
Qy 541 GACGCTGAAGATAGTGTGAAAACATGATCAATTTGAAATGGCATCCCTCTGATCCC 600
Db 572 GACGCTGAAGATAGTGTGAAAACATGATCAATTTGAAATGGCATCCCTCTGATCCC 631
Qy 601 CTGACATGAGAGGG-GGGCAATTTATGATGCTTCATG 638
Db 632 CTGACATGAGAGGGCAATTTATGATGCTTCATG 670

RESULT 14
LOCUS BD247957 848 bp DNA linear PAT 17-JUL-2003
DEFINITION 5' ESTs for secreted proteins expressed in various tissues.
ACCESSION BD247957
VERSION BD247957.1 GI:33057727
KEYWORDS JP 2002525024-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 848)
REFERENCE Edwards, J.B.D.M., Duclet, A. and Lacroix, B.
AUTHORS 5' ESTs for secreted proteins expressed in various tissues
TITLE Patent: JP 2002525024-A 22 13-AUG-2002;
JOURNAL GENESET
COMMENT OS Homo sapiens (human)
PN JP 2002525024-A/22
PD 13-AUG-2002
PR 31-JUL-1998 JP 2000505294
PI 01-AUG-1997 US 08/905051
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLET, BRUNO PI
LACROIX
PC C12N15/09, C12N15/09, C07K14/47, C12M1/00, C12P21/02, C12N15/00, PC
C12N15/00
CC Von Heijne matrix
CC score 10.7
CC seq LMLPFLVTAHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32..73.
Location/Qualifiers
1..848
/organism="Homo sapiens"

ORIGIN /mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGTTGCTGCTCTTTTCTGTTGAGCTGCTCATTCATGCTGACTCTGTCAACCAAGT 60
Db 32 ATGTTGCTGCTCTTTTCTGTTGAGCTGCTCATTCATGCTGACTCTGTCAACCAAGT 91
Qy 61 GAGAAATGCTTTTAAAGTAGAGCTTAGATCAAGAACGCTCTGGAGATTAAAGCATAT 120
Db 92 GAGAAATGCTTTTAAAGTAGAGCTTAGATCAAGAACGCTCTGGAGATTAAAGCATAT 151
Qy 121 GCTGGATACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 180
Db 152 GCTGGATACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 211
Qy 181 GTTCCCAAGAGAGCAACAGAAATTTCCCATGTCCTTCACTTTGCAATGTAAACCGAGG 240
Db 212 GTTCCCAAGAGAGCAACAGAAATTTCCCATGTCCTTCACTTTGCAATGTAAACCGAGG 271
Qy 241 GATATCTTGTGTTTGTGTTTACAGACCTTCAAAAATCAACCCCTTCTGTGTAG 300
Db 272 GATATCTTGTGTTTGTGTTTACAGACCTTCAAAAATCAACCCCTTCTGTGTAG 331
Qy 301 GGCATACGACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 360
Db 332 GTGCAATACGACCAATGAAGAAATACCTCTTCAAGACGATGGTAGCTTTCATGAGAAA 391
Qy 361 CAACTCTGGAATTTTAAATATCCCTTCACACTTGCACACCCATGACCCATCTGTG 420
Db 392 CAACTCTGGAATTTTAAATATCCCTTCACACTTGCACACCCATGACCCATCTGTG 451
Qy 421 CCCATCTGATTTATATATTTGGTGTGATTTTGTGATCATCATAGTGAATTGACAT 480
Db 452 CCCATCTGATTTATATATTTGGTGTGATTTTGTGATCATCATAGTGAATTGACAT 511
Qy 481 CTGATTTTATCAGGAGCTGCGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 512 CTGATTTTATCAGGAGCTGCGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAG 571
Qy 541 GACGCTGAAGATAGTGTGAAAACATGATCAATTTGAAATGGCATCCCTCTGATCCC 600
Db 572 GACGCTGAAGATAGTGTGAAAACATGATCAATTTGAAATGGCATCCCTCTGATCCC 631
Qy 601 CTGACATGAGAGGG-GGGCAATTTATGATGCTTCATG 638
Db 632 CTGACATGAGAGGGCAATTTATGATGCTTCATG 670

RESULT 15
LOCUS AR340701 848 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 27 from patent US 6573068.
ACCESSION AR340701
VERSION AR340701.1 GI:33732443
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 848)
AUTHORS Milne Edwards, J.-B.D., Duclet, A. and Bougueleret, L.
TITLE Claudin-50 protein
JOURNAL Patent: US 6573068-A 27 03-JUN-2003;
FEATURES Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ATGTTGGCTGCTCTCTTTTCTGTTGAGCTGCAATTCATGCTGAACTGTGCAACGAGT 60
DB 32 ATGTTGGCTGCTCTCTTTTCTGTTGAGCTGCAATTCATGCTGAACTGTGCAACGAGT 91
QY 61 GCAGAAAATGCTTTTAAAGTGAGACTTATGATCAAGACGCTTGGAGATTAAGCATAT 120
DB 92 GCAGAAAATGCTTTTAAAGTGAGACTTATGATCAAGACGCTTGGAGATTAAGCATAT 151
QY 121 GCCTGGATACCAATGAAGATATACCTCTCAAGAGAGATGATGCTTCTCATAGAAAA 180
DB 152 GCCTGGATACCAATGAAGATATACCTCTCAAGAGAGATGATGCTTCTCATAGAAAA 211
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCCTAATTGCAATGTAACCCAGAG 240
DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCCTAATTGCAATGTAACCCAGAG 271
QY 241 GTATCATTCCTGTTGTGTTGATCAAGACCTTCAAAAAATCAACCTTCTGCTGTGAG 300
DB 272 GTATCATTCCTGTTGTGTTGATCAAGACCTTCAAAAAATCAACCTTCTGCTGTGAG 331
QY 301 GTGCAATGAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAATGAC 360
DB 332 GTGCAATGAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAATGAC 391
QY 361 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACCAACCCATGAGCCATCTGTG 420
DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACCAACCCATGAGCCATCTGTG 451
QY 421 CCCATCTGATATTAATATTTGTTGATATTTTGCATATCATATGTCATATTCAGACTA 480
DB 452 CCCATCTGATATTAATATTTGTTGATATTTTGCATATCATATGTCATATTCAGACTA 511
QY 481 CTGATTTTATCAGGATCTGCGCAAGTGAAGAAACAAAGAACCATCTGAATGAT 540
DB 512 CTGATTTTATCAGGATCTGCGCAAGTGAAGAAACAAAGAACCATCTGAATGAT 571
QY 541 GACGCTGAAGATTAAGTGAAGAAACATGATCAATGTAAGAAATGCTCTGATGCC 600
DB 572 GACGCTGAABATTAATGTAAGAAACATGATCAATGTAAGAAATGCTCTGATGCC 631
QY 601 CTGACATGAAGGG-GGGCATTTTAATGATGCTTCATG 638
DB 632 CTGACATGAAGGGGAGGATTAATGATGCTTCATG 670
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RESULT 16
LOCUS AR412373 848 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6639063.
ACCESSION AR412373
VERSION AR412373.1 GI:40167483
KEYWORDS
ORGANISM Unknown.
SOURCE Unknown.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards, J.-B. D. M., Jobert, S. and Giordano, J.-Y.
TITLE BSR's and encoded human proteins
JOURNAL Patent: US 6639063-A 5 28-OCT-2003;
FEATURES
source Location/Qualifiers
1..848
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTTGGCTGCTCTCTTTTCTGTTGAGCTGCAATTCATGCTGAACTGTGCAACGAGT 60
DB 32 ATGTTGGCTGCTCTCTTTTCTGTTGAGCTGCAATTCATGCTGAACTGTGCAACGAGT 91

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QY 61 GCAGAAAATGCTTTTAAAGTGAGACTTATGATCAAGACGCTTGGAGATTAAGCATAT 120
DB 92 GCAGAAAATGCTTTTAAAGTGAGACTTATGATCAAGACGCTTGGAGATTAAGCATAT 151
QY 121 GCCTGGATACCAATGAAGATATACCTCTCAAGAGAGATGATGCTTCTCATAGAAAA 180
DB 152 GCCTGGATACCAATGAAGATATACCTCTCAAGAGAGATGATGCTTCTCATAGAAAA 211
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCCTAATTGCAATGTAACCCAGAG 240
DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCATGTCCTAATTGCAATGTAACCCAGAG 271
QY 241 GTATCATTCCTGTTGTGTTGATCAAGACCTTCAAAAAATCAACCTTCTGCTGTGAG 300
DB 272 GTATCATTCCTGTTGTGTTGATCAAGACCTTCAAAAAATCAACCTTCTGCTGTGAG 331
QY 301 GTGCAATGAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAATGAC 360
DB 332 GTGCAATGAGCCATTAAGATGAAGAACGAGATCAACATGCTTCTTCTTAATGAC 391
QY 361 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACCAACCCATGAGCCATCTGTG 420
DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACCAACCCATGAGCCATCTGTG 451
QY 421 CCCATCTGATATTAATATTTGTTGATATTTTGCATATCATATGTCATATTCAGACTA 480
DB 452 CCCATCTGATATTAATATTTGTTGATATTTTGCATATCATATGTCATATTCAGACTA 511
QY 481 CTGATTTTATCAGGATCTGCGCAAGTGAAGAAACAAAGAACCATCTGAATGAT 540
DB 512 CTGATTTTATCAGGATCTGCGCAAGTGAAGAAACAAAGAACCATCTGAATGAT 571
QY 541 GACGCTGAAGATTAAGTGAAGAAACATGATCAATGTAAGAAATGCTCTGATGCC 600
DB 572 GACGCTGAABATTAATGTAAGAAACATGATCAATGTAAGAAATGCTCTGATGCC 631
QY 601 CTGACATGAAGGG-GGGCATTTTAATGATGCTTCATG 638
DB 632 CTGACATGAAGGGGAGGATTAATGATGCTTCATG 670
```

RESULT 17
LOCUS AX884142 848 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from Patent EP1033401.
ACCESSION AX884142
VERSION AX884142.1 GI:40039026
KEYWORDS
ORGANISM Homo sapiens (human)
SOURCE Homo sapiens
REFERENCE 1 (bases 1 to 848)
AUTHORS Dumas, M. L., Edwards, J. B., Ducle, A. and Giordano, J. Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 5 06-SEP-2000;
FEATURES
source Location/Qualifiers
1..848
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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32..700
/note="unnamed protein product"
/codon_start=1
/protein_id="CA93778.1"
/db_xref="GI:40039027"
/translation="MMLFLVLTALHMLCPGAEANFKVLSIFALGDKAYANDT
NREYLFKAVAPSMKRVPRVREATRISHVLICNVYQKVSFVFTDPSKHTLLPAVEVQ

SAIRNKRNINNAFFLNDQTLFPLKIPSTLAPPMDSPYIWIIRGIFCIITVAIAL
LILSGIWMKXKXKSESYDABXCEMMITLENGIPSPDLMKSGSHINDAPMTBDR
LTPPL"
32..73
/note="Von Heijne matrix"

ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ATGTTGCTGCTCTCTTTTCTGCTGACCTTCATGCTGAACCTCTGTCAACGAT 60
DB |||
DB 32 ATGTTGCTGCTCTCTTTTCTGCTGACCTTCATGCTGAACCTCTGTCAACGAT 91
QY 61 GAGAGAAAGCTTTTAAAGTGAAGTCTAGTACAGAAAGCTCTGGAGATAAGCATAT 120
DB |||
DB 92 GAGAGAAAGCTTTTAAAGTGAAGTCTAGTACAGAAAGCTCTGGAGATAAGCATAT 151
QY 121 GCTGGAGATACCAATGAAATACCTCTTCAAGAGATGATGCTTCTCCATGAGAAA 180
DB |||
DB 152 GCTGGAGATACCAATGAAATACCTCTTCAAGAGATGATGCTTCTCCATGAGAAA 211
QY 181 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTACTTTCATGATGATGATGAT 240
DB |||
DB 212 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTACTTTCATGATGATGATGAT 271
QY 241 GTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB |||
DB 272 GTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
QY 301 GTGCATCAGCCATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT 360
DB |||
DB 332 GTGCATCAGCCATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT 391
QY 361 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGAGACCATCTG 420
DB |||
DB 392 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGAGACCATCTG 451
QY 421 CCCATCTGATATATATATATATATATATATATATATATATATATATATATAT 480
DB |||
DB 452 CCCATCTGATATATATATATATATATATATATATATATATATATATATATAT 511
QY 481 CTGATTTTATCAGGATCTGCAAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAT 540
DB |||
DB 512 CTGATTTTATCAGGATCTGCAAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAT 571
QY 541 GAGCTGAAGATTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATG 600
DB |||
DB 572 GAGCTGAAGATTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATG 631
QY 601 CTGACATGAGAGG-AGGCAATTAATGATGATGATGATGATGATGATGATG 638
DB |||
DB 632 CTGACATGAGAGGAGGCAATTAATGATGATGATGATGATGATGATGATG 670
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RESULT 18

BD023757 848 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD023757
VERSION BD023757.1 GI:22564980
KEYWORDS JP 2001269182-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Edwards, J.B.D.M., Duclair, R. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein.
JOURNAL Patent: JP 2001269182-A 3 02-OCT-2001;

COMMENT OS Homo sapiens (human)

PN JP 2001269182-A/3
PD 02-OCT-2001
PR 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC Von Heijne matrix
FH Key 32..697
FT CDS 32..73.
FT sig_peptide 32..73.
FEATURES
Location/Qualifiers
1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ATGTTGCTGCTCTCTTTTCTGCTGACCTTCATGCTGAACCTCTGTCAACGAT 60
DB |||
DB 32 ATGTTGCTGCTCTCTTTTCTGCTGACCTTCATGCTGAACCTCTGTCAACGAT 91
QY 61 GAGAGAAAGCTTTTAAAGTGAAGTCTAGTACAGAAAGCTCTGGAGATAAGCATAT 120
DB |||
DB 92 GAGAGAAAGCTTTTAAAGTGAAGTCTAGTACAGAAAGCTCTGGAGATAAGCATAT 151
QY 121 GCTGGAGATACCAATGAAATACCTCTTCAAGAGATGATGCTTCTCCATGAGAAA 180
DB |||
DB 152 GCTGGAGATACCAATGAAATACCTCTTCAAGAGATGATGCTTCTCCATGAGAAA 211
QY 181 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTACTTTCATGATGATGATGAT 240
DB |||
DB 212 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTACTTTCATGATGATGATGAT 271
QY 241 GTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB |||
DB 272 GTATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 331
QY 301 GTGCATCAGCCATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT 360
DB |||
DB 332 GTGCATCAGCCATAGATAGATAGATAGATAGATAGATAGATAGATAGATAGAT 391
QY 361 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGAGACCATCTG 420
DB |||
DB 392 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGCACACCCATGAGACCATCTG 451
QY 421 CCCATCTGATATATATATATATATATATATATATATATATATATATATATAT 480
DB |||
DB 452 CCCATCTGATATATATATATATATATATATATATATATATATATATATATAT 511
QY 481 CTGATTTTATCAGGATCTGCAAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAT 540
DB |||
DB 512 CTGATTTTATCAGGATCTGCAAGCTAGAGAGAGAGAGAGAGAGAGAGAGAGAT 571
QY 541 GAGCTGAAGATTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATG 600
DB |||
DB 572 GAGCTGAAGATTAAGTGAAGAGATGATGATGATGATGATGATGATGATGATG 631
QY 601 CTGACATGAGAGG-AGGCAATTAATGATGATGATGATGATGATGATGATG 638
DB |||
DB 632 CTGACATGAGAGGAGGCAATTAATGATGATGATGATGATGATGATGATG 670
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RESULT 19

BD073618 848 bp DNA linear PAT 27-AUG-2002
LOCUS

DEFINITION 5'EST of secreted protein expressing in testis and other tissues.
ACCESSION BD073618
VERSION BD073618.1 GI:22619221
KEYWORDS JP 2001512012-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Baputist,D.M.B.D., Bimeric,D. and Bruno,L.
TITLE 5'EST of secreted protein expressing in testis and other tissues
JOURNAL Patent: JP 2001512012-A 22 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512012-A/22
PD 21-AUG-2001
PR 31-JUL-1998 JP 2000505290
PI 01-AUG-1997 US 08/305279
PI DUMAS MILNE EDWARDS JEAN BAPTIST,DUCLAIR EIMERIC,IACROIX PI
BRUNO
PC C12N15/09,A61K38/00,A61K48/00,C07K14/435,C07K19/00,C12P21/02,
PC C12Q1/68,
PC G01N33/50,G01N33/53,G01N33/566,C12N15/00,A61K37/02
CC Strandedness: Double;
CC Topology: Linear;
CC score 10.7
CC seq LMILFLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32..73.
Location/Qualifiers
FEATURES
source 1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred.No.9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGTTGGGCTGCTCTTTTCTGTCGACCTGCACTGTCGAACTCTGTCACCAAGT 60
DB 32 ATGTTGGGCTGCTCTTTTCTGTCGACCTGCACTGTCGAACTCTGTCACCAAGT 91
QY 61 GCAGAAATGCTTTTAAAGTGAAGTCTTATCGAAGCAGCTCTGGAGATTAACATAT 120
DB 92 GCAGAAATGCTTTTAAAGTGAAGTCTTATCGAAGCAGCTCTGGAGATTAACATAT 151
QY 121 GCTGGATACCAATGAAGATACCTCTTCAAGGATGTAGCTTTCTCCATGAGAAA 180
DB 152 GCTGGATACCAATGAAGATACCTCTTCAAGGATGTAGCTTTCTCCATGAGAAA 211
QY 181 GTTCCCAAGAGAGCAAGAAATTTCCATGTCCTTACTTGTCAATGTAAACCAAGG 240
DB 212 GTTCCCAAGAGAGCAAGAAATTTCCATGTCCTTACTTGTCAATGTAAACCAAGG 271
QY 241 GTATCATTCGTTTGTGTTACAGACCTTCAAAAATCAACCTTCCGCTGTAG 300
DB 272 GTATCATTCGTTTGTGTTACAGACCTTCAAAAATCAACCTTCCGCTGTAG 331
QY 301 GTGCATCAGCATAGATGAAGATACCTCTTCAAGGATGTAGCTTTCTTAAATGAC 360
DB 332 GTGCATCAGCATAGATGAAGATACCTCTTCAAGGATGTAGCTTTCTTAAATGAC 391
QY 361 CAAACTGTGAATTTTAAATATCCCTTCCACACTTGTGACCAACCATGAGCCATCTGTG 420
DB 392 CAAACTGTGAATTTTAAATATCCCTTCCACACTTGTGACCAACCATGAGCCATCTGTG 451
QY 421 CCATCTGGAATTTTAAATATCCCTTCCACACTTGTGACCAACCATGAGCCATCTGTG 480
DB 452 CCATCTGGAATTTTAAATATCCCTTCCACACTTGTGACCAACCATGAGCCATCTGTG 511
QY 481 CTGATTTATCAGGATCTGGCAAGTGAAGAAAGAAAGAAAGCAATCTGAAGTGAAT 540

DB 512 CTGATTTATCAGGATCTGGCAAGTGAAGAAAGAAAGCAATCTGAAGTGAAT 571
QY 541 GACGCTGAAGATTAAGTGAAGAAAGTGAATGAATGAATGAATGATCCCTGATGCC 600
DB 572 GACGCTGAAGATTAAGTGAAGAAAGTGAATGAATGAATGATCCCTGATGCC 631
QY 601 CTGACATGAAGAGG-GGGCATTTATGATGATGCTTCATG 638
DB 632 CTGACATGAAGAGGAGGATTTATGATGATGCTTCATG 670
RESULT 20
BD075896 848 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION 5' EST of secretory protein expressed in endoblast.
ACCESSION BD075896
VERSION BD075896.1 GI:22621499
KEYWORDS JP 2001512005-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Duclet,A. and Lacroix,B.
TITLE 5' EST of secretory protein expressed in endoblast
JOURNAL Patent: JP 2001512005-A 22 21-AUG-2001;
GENSET
COMMENT OS Homo sapiens (human)
PN JP 2001512005-A/22
PD 21-AUG-2001
PR 31-JUL-1998 JP 2000505194
PI 01-AUG-1997 US 08/304468
PI JEAN BAPTISTE DUMAS MILNE EDWARDS,AYMERIC DUCLETT, BRUNO PI
LACROIX
PC C12N15/09,C07K19/00,C12M1/00,C12N1/15,C12N1/19,C12N1/21,C12N5/09,
PC C12Q1/68,
PC C12N15/00,C12N5/00
CC Von Heijne matrix
CC score 10.7
CC seq LMILFLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32..73.
Location/Qualifiers
FEATURES
source 1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred.No.9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
QY 1 ATGTTGGGCTGCTCTTTTCTGTCGACCTGCACTGTCGAACTCTGTCACCAAGT 60
DB 32 ATGTTGGGCTGCTCTTTTCTGTCGACCTGCACTGTCGAACTCTGTCACCAAGT 91
QY 61 GCAGAAATGCTTTTAAAGTGAAGTCTTATCGAAGCAGCTCTGGAGATTAACATAT 120
DB 92 GCAGAAATGCTTTTAAAGTGAAGTCTTATCGAAGCAGCTCTGGAGATTAACATAT 151
QY 121 GCTGGATACCAATGAAGATACCTCTTCAAGGATGTAGCTTTCTCCATGAGAAA 180
DB 152 GCTGGATACCAATGAAGATACCTCTTCAAGGATGTAGCTTTCTCCATGAGAAA 211
QY 181 GTTCCCAAGAGAGCAAGAAATTTCCATGTCCTTACTTGTCAATGTAAACCAAGG 240
DB 212 GTTCCCAAGAGAGCAAGAAATTTCCATGTCCTTACTTGTCAATGTAAACCAAGG 271
QY 241 GTATCATTCGTTTGTGTTACAGACCTTCAAAAATCAACCTTCCGCTGTAG 300
DB 272 GTATCATTCGTTTGTGTTACAGACCTTCAAAAATCAACCTTCCGCTGTAG 331

QY 301 GTGCATCAGCCATAGAAAGAAACCGATCAATGCTCTTCTTAATGAC 360
DB 332 GTGCATCAGCCATAGAAAGAAACCGATCAATGCTCTTCTTAATGAC 391
QY 361 CAAACTGTGAATTTTAAATCCCTTCCACACTTGCACCCCATGAGCCATCTGTG 420
DB 392 CAAACTGTGAATTTTAAATCCCTTCCACACTTGCACCCCATGAGCCATCTGTG 451
QY 421 CCCATCTGATTTTATTTATTTGGTGAATTTTTCATCATGATGGAATGCACTA 480
DB 452 CCCATCTGATTTTATTTATTTGGTGAATTTTTCATCATGATGGAATGCACTA 511
QY 481 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAACCATCTGAAGTGGAT 540
DB 512 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAACCATCTGAAGTGGAT 571
QY 541 GAGCTGAAGATTAAGTGTGAAGAAACATGATCAATTTGAAATGCGATCCCTCTGATCCC 600
DB 572 GAGCTGAAGATTAAGTGTGAAGAAACATGATCAATTTGAAATGCGATCCCTCTGATCCC 631
QY 601 CTGACATGAAGGG-GGGCATATTATTAATGATCCCTTCATG 638
DB 632 CTGACATGAAGGGAGGGCATATTATTAATGATCCCTTCATG 670

RESULT 21
BD076074 848 bp DNA linear PAT 27-AUG-2002
LOCUS BD076074
DEFINITION 5' EST of tissue-nonspecific secretory protein.
ACCESSION BD076074.1 GI:22621677
VERSION JP 2001512011-A/22.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Edwards J.B.D.M., Duclet A. and Lacroix B.
AUTHORS 1 (bases 1 to 848)
TITLE 5' EST of tissue-nonspecific secretory protein
JOURNAL Patent: JP 2001512011-A 22 21-AUG-2001;
GENSBT

COMMENT OS Homo sapiens (human)
PN JP 2001512011-A/22
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505289
PR 01-AUG-1997 US 08/905135
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLETT, BRUNO PI
LACROIX
PC C12N15/09, C12N15/09, C07K14/47, C12Q1/68, C12N15/00, C12N15/00 CC
Von Heijne matrix
CC score 10.7
CC seq LMLPLPLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32..73.
Location/Qualifiers
1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162; Indels 1; Gaps 1;
Matches 634; Conservative 4; Mismatches 0;

QY 1 ATGTTGGCTGCTCTTTTCTGTGACCTGCAATGCTGCAACTCTGCAACGAGT 60
DB 32 ATGTTGGCTGCTCTTTTCTGTGACCTGCAATGCTGCAACTCTGCAACGAGT 91
QY 61 GCAGAAATGCTTTAAAGTGAAGTATGATCAAGACGCTCTGGAGATTAAGCATAT 120
DB 92 GCAGAAATGCTTTAAAGTGAAGTATGATCAAGACGCTCTGGAGATTAAGCATAT 151

QY 121 GCTGGATACCAATGAGATACCTCTTCAAGCGATGTAAGTCTTCTCCATGAGAAA 180
DB 152 GCTGGATACCAATGAGATACCTCTTCAAGCGATGTAAGTCTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCCATGCTCTTACTTTGCAATGTAACGAGG 240
DB 212 GTTCCCAACAGAGAGCAAGAAATTTCCCATGCTCTTACTTTGCAATGTAACGAGG 271
QY 241 GTATCATCTGTTTGTGTTACAGACCTTCAAAATATCAACCTTCTGCTGTGAG 300
DB 272 GTATCATCTGTTTGTGTTACAGACCTTCAAAATATCAACCTTCTGCTGTGAG 331
QY 301 GTGCATCAGCCATAGAAAGAAACCGATCAATGCTCTTCTTAATGAC 360
DB 332 GTGCATCAGCCATAGAAAGAAACCGATCAATGCTCTTCTTAATGAC 391
QY 361 CAAACTGTGAATTTTAAATCCCTTCCACACTTGCACCCCATGAGCCATCTGTG 420
DB 392 CAAACTGTGAATTTTAAATCCCTTCCACACTTGCACCCCATGAGCCATCTGTG 451
QY 421 CCCATCTGATTTTATTTATTTGGTGAATTTTTCATCATGATGGAATGCACTA 480
DB 452 CCCATCTGATTTTATTTATTTGGTGAATTTTTCATCATGATGGAATGCACTA 511
QY 541 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAACCATCTGAAGTGGAT 540
DB 572 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAACCATCTGAAGTGGAT 571
QY 541 GAGCTGAAGATTAAGTGTGAAGAAACATGATCAATTTGAAATGCGATCCCTCTGATCCC 600
DB 572 GAGCTGAAGATTAAGTGTGAAGAAACATGATCAATTTGAAATGCGATCCCTCTGATCCC 631
QY 601 CTGACATGAAGGG-GGGCATATTATTAATGATCCCTTCATG 638
DB 632 CTGACATGAAGGGAGGGCATATTATTAATGATCCCTTCATG 670

RESULT 22
BD076775 848 bp DNA linear PAT 27-AUG-2002
LOCUS BD076775
DEFINITION 5' EST of secretory protein expressed in prostate.
ACCESSION BD076775.1 GI:22622378
VERSION JP 2001512013-A/22.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE Edwards J.B.D.M., Duclet A. and Lacroix B.
AUTHORS 1 (bases 1 to 848)
TITLE 5' EST of secretory protein expressed in prostate
JOURNAL Patent: JP 2001512013-A 22 21-AUG-2001;
GENSBT

COMMENT OS Homo sapiens (human)
PN JP 2001512013-A/22
PD 21-AUG-2001
PF 31-JUL-1998 JP 2000505291
PR 01-AUG-1997 US 08/905144
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLETT, BRUNO PI
LACROIX
PC C12N15/09, C07K14/47, C12P21/02, C12Q1/02, C12Q1/68, C12N15/00 CC
Von Heijne matrix
CC score 10.7
CC seq LMLPLPLVTAIHA/EL
FH Key Location/Qualifiers
FT sig_peptide 32..73.
Location/Qualifiers
1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
 Best Local Similarity 99.2%; Pred. No. 9.3e-162;
 Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ATGTTGTCGCTCTCTTTTCTGTCGTCGTCATTCATCTGTAACCTCTGTCAACAGGT 60
   |||||
DB 32 ATGTTGTCGCTCTCTTTTCTGTCGTCGTCATTCATCTGTAACCTCTGTCAACAGGT 91
   |||||
QY 61 GCAGAAAATGCTTTTAAAGTAGAGCTTAGTACAGAACGCTCTGAGATTAAGCATAT 120
   |||||
DB 92 GCAGAAAATGCTTTTAAAGTAGAGCTTAGTACAGAACGCTCTGAGATTAAGCATAT 151
   |||||
QY 121 GCCTGGATACCAATGAGAAATACCTCTTCAAGAGATGTAAGTCTTCTCATGAGAAA 180
   |||||
DB 152 GCCTGGATACCAATGAGAAATACCTCTTCAAGAGATGTAAGTCTTCTCATGAGAAA 211
   |||||
QY 181 GTTCCCAAGAGAAAGCAAGAAATTTCCATGTCTTCACTTTCAGATGTAAACCAAGAG 240
   |||||
DB 212 GTTCCCAAGAGAAAGCAAGAAATTTCCATGTCTTCACTTTCAGATGTAAACCAAGAG 271
   |||||
QY 241 GTATCATCTGCTGTTGTTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 300
   |||||
DB 272 GTATCATCTGCTGTTGTTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 331
   |||||
QY 301 GTGCAATCAGCATTAAGATGAAACAAGAACCGATCAACATGCTCTTCTTAAATGAC 360
   |||||
DB 332 GTGCAATCAGCATTAAGATGAAACAAGAACCGATCAACATGCTCTTCTTAAATGAC 391
   |||||
QY 361 CAAACTCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 420
   |||||
DB 392 CAAACTCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 451
   |||||
QY 421 CCCATCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 480
   |||||
DB 452 CCCATCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 511
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QY 481 CTGATTTTATCAGGATCTGCGACGCTAGAGAAAGAAACAACATCTGAAGTGAT 540
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DB 512 CTGATTTTATCAGGATCTGCGACGCTAGAGAAAGAAACAACATCTGAAGTGAT 571
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QY 541 GACGCTGAGATTAAGTGTGAAAACATGATCACAATGGAATGCAATCCCTCTGATGCC 600
   |||||
DB 572 GACGCTGAGATTAAGTGTGAAAACATGATCACAATGGAATGCAATCCCTCTGATGCC 631
   |||||
QY 601 CTGACATGAAAGGG-GGGCATTTAATGATGCTTCATG 638
   |||||
DB 632 CTGACATGAAAGGGGCGCATTTAATGATGCTTCATG 670
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```

RESULT 23

BD077436

LOCUS

848 bp

DNA

linear

PAT 27-AUG-2002

DEFINITION 5'EST of secreted protein expressed in muscles and other mesodermal tissues.

ACCESSION

BD077436

VERSION

BD077436.1

KEYWORDS

JP 2001512016-A/22

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

TITLE

1 (bases 1 to 848)

Edwards, J.B.D.M., Duclert, A. and Lacroix, B.

5'EST of secreted protein expressed in muscles and other mesodermal

tissues

JOURNAL

GENSET

PATENT: JP 2001512016-A 22 21-AUG-2001;

COMMENT

OS

Homo sapiens (human)

PN

JP 2001512016-A/22

PD

21-AUG-2001

PF

31-JUL-1998 JP 2000505295

PR

01-AUG-1997 US 08/905134

PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AMERIC DUCLERT, BRUNO PI
 LACROIX
 PC C12N15/09, C12N15/09, C07K14/47, C12M1/00, C12N15/00, C12N15/00 CC
 Von Heljne matrix
 CC Score 10.7
 FH Key Location/Qualifiers
 FT s19_peptide 32..73.
 Location/Qualifiers
 1..848
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 98.0%; Score 625; DB 6; Length 848;
 Best Local Similarity 99.2%; Pred. No. 9.3e-162;
 Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ATGTTGTCGCTCTCTTTTCTGTCGTCGTCATTCATCTGTAACCTCTGTCAACAGGT 60
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DB 32 ATGTTGTCGCTCTCTTTTCTGTCGTCGTCATTCATCTGTAACCTCTGTCAACAGGT 91
   |||||
QY 61 GCAGAAAATGCTTTTAAAGTAGAGCTTAGTACAGAACGCTCTGAGATTAAGCATAT 120
   |||||
DB 92 GCAGAAAATGCTTTTAAAGTAGAGCTTAGTACAGAACGCTCTGAGATTAAGCATAT 151
   |||||
QY 121 GCCTGGATACCAATGAGAAATACCTCTTCAAGAGATGTAAGTCTTCTCATGAGAAA 180
   |||||
DB 152 GCCTGGATACCAATGAGAAATACCTCTTCAAGAGATGTAAGTCTTCTCATGAGAAA 211
   |||||
QY 181 GTTCCCAAGAGAAAGCAAGAAATTTCCATGTCTTCACTTTCAGATGTAAACCAAGAG 240
   |||||
DB 212 GTTCCCAAGAGAAAGCAAGAAATTTCCATGTCTTCACTTTCAGATGTAAACCAAGAG 271
   |||||
QY 241 GTATCATCTGCTGTTGTTGTTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 300
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   |||||
QY 361 CAAACTCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 420
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   |||||
QY 421 CCCATCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 480
   |||||
DB 452 CCCATCTGGAATTTTAAATATCCCTTCCACATTCGACACCAATGAGACCATCTGTG 511
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QY 481 CTGATTTTATCAGGATCTGCGACGCTAGAGAAAGAAACAACATCTGAAGTGAT 540
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DB 512 CTGATTTTATCAGGATCTGCGACGCTAGAGAAAGAAACAACATCTGAAGTGAT 571
   |||||
QY 541 GACGCTGAGATTAAGTGTGAAAACATGATCACAATGGAATGCAATCCCTCTGATGCC 600
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DB 572 GACGCTGAGATTAAGTGTGAAAACATGATCACAATGGAATGCAATCCCTCTGATGCC 631
   |||||
QY 601 CTGACATGAAAGGG-GGGCATTTAATGATGCTTCATG 638
   |||||
DB 632 CTGACATGAAAGGGGCGCATTTAATGATGCTTCATG 670
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```

RESULT 24

BD077737

LOCUS

848 bp

DNA

linear

PAT 27-AUG-2002

DEFINITION 5'EST of secretory protein in brain.

ACCESSION

BD077737

VERSION

BD077737.1

KEYWORDS

JP 2001512015-A/22

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 848)
Edwards, J. B. D. M., Ducleert, A. and Lacroix, B.
5'EST of secretory protein in brain
Patent: JP 2001512015-A 22 21-AUG-2001;
GENEST
COMMENT
OS Homo sapiens (human)
PN JP 2001512015-A/22
PD 21-AUG-2001
PF 31-JUN-1998 JP 2000505293
PR 01-AUG-1997 US 08/905223
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLEERT, BRUNO PI LACROIX
PC C12N15/09, C07K14/47, C12M1/00, C12P21/02, C12Q1/68, C12N15/00 CC
Von Heijne matrix
CC score 10.7
FH key Location/Qualifiers
FT sig_peptide 32..73.
Location/Qualifiers
1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162; Indels 1; Gaps 1;
Matches 634; Conservative 4; Mismatches 0;
1 ATGTTGCGCTGCTCTTTTCTGTTGAGTGCATTCATGCTGAACTCTGTCAACGAGT 60
32 ATGTTGCGCTGCTCTTTTCTGTTGAGTGCATTCATGCTGAACTCTGTCAACGAGT 91
61 GCAGAAATGCTTTTAAAGTGAAGTATGATTCAGAACACTCTGGAGATTAAGCATAT 120
92 GCAGAAATGCTTTTAAAGTGAAGTATGATTCAGAACACTCTGGAGATTAAGCATAT 151
121 GCGTGGATACCAATGAAGATACCTCTCAAGACATGTTGCTTCATGAGAAA 180
152 GCGTGGATACCAATGAAGATACCTCTCAAGACATGTTGCTTCATGAGAAA 211
181 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTCAATGTAACCAAGAG 240
212 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTCAATGTAACCAAGAG 271
241 GATCATCTGCTGTTGTTAAGACCTTCAAAAATGACACCTCTGCTGTTGAG 300
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392 CAAACTCTGGAATTTTAAATCCCTTCCACTTGACCAACCAATGAGCCATCTG 451
421 CCCATCTGATTAATTAATTTGTTGATATTTTGCATCATATGTTGCAATTCAC 480
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481 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACCAATCTGAAGGAT 540
512 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACCAATCTGAAGGAT 571
541 GAGCGTGAAGATTAAGTGAAGAACATGATCAATTTGAATGAGCATCCCTCTGATCCC 600
572 GAGCGTGAAGATTAAGTGAAGAACATGATCAATTTGAATGAGCATCCCTCTGATCCC 631
601 CTGGAATGAAGG-GGCATATTAATGATGCTTCATG 638
|||||

Db 632 CTGGAATGAAGGAGGATTAATGATGCTTCATG 670
RESULT 25
BD085880 848 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 848)
Bougueleret, L., Ducleert, A. and Edwards, J. B. D. M.
Blongation cDNA of secretory protein
Patent: JP 2001523453-A 22 27-NOV-2001;
GENEST
COMMENT
OS Homo sapiens (human)
PN JP 2001523453-A/22
PD 27-NOV-2001
PF 13-NOV-1998 JP 2000521191
PR 13-NOV-1997 US 60/066677, 17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121, 13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116, 04-SEP-1998 US 60/092273 PI
BOUGUELERET, AYMERIC DUCLEERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
Von Heijne matrix
FH key Location/Qualifiers
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Location/Qualifiers
1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162; Indels 1; Gaps 1;
Matches 634; Conservative 4; Mismatches 0;
1 ATGTTGCGCTGCTCTTTTCTGTTGAGTGCATTCATGCTGAACTCTGTCAACGAGT 60
32 ATGTTGCGCTGCTCTTTTCTGTTGAGTGCATTCATGCTGAACTCTGTCAACGAGT 91
61 GCAGAAATGCTTTTAAAGTGAAGTATGATTCAGAACACTCTGGAGATTAAGCATAT 120
92 GCAGAAATGCTTTTAAAGTGAAGTATGATTCAGAACACTCTGGAGATTAAGCATAT 151
121 GCGTGGATACCAATGAAGATACCTCTCAAGACATGTTGCTTCATGAGAAA 180
152 GCGTGGATACCAATGAAGATACCTCTCAAGACATGTTGCTTCATGAGAAA 211
181 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTCAATGTAACCAAGAG 240
212 GTTCCCAAGAGAACCAAGAAATTTCCATGCTCTTCAATGTAACCAAGAG 271
241 GATCATCTGCTGTTGTTAAGACCTTCAAAAATGACACCTCTGCTGTTGAG 300
272 GATCATCTGCTGTTGTTAAGACCTTCAAAAATGACACCTCTGCTGTTGAG 331
301 GTGCAATCAGCCATGAAGTAAAGAACCGGATCAACATGCTCTTCTAAATGAC 360
332 GTGCAATCAGCCATGAAGTAAAGAACCGGATCAACATGCTCTTCTAAATGAC 391
361 CAAACTCTGGAATTTTAAATCCCTTCCACTTGACCAACCAATGAGCCATCTG 420
392 CAAACTCTGGAATTTTAAATCCCTTCCACTTGACCAACCAATGAGCCATCTG 451
421 CCCATCTGATTAATTAATTTGTTGATATTTTGCATCATATGTTGCAATTCAC 480
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Db 452 CCCATCTGGATTATTAATTTGGTGTATATTTGCAATCATCATGATGGCAATTGCACTA 511
Qy 481 CTGATTTTATCAGGAGCTGGCAAGTAAAGAAAGAAAGAAAGCAATCTGAAGTGAAT 540
Db 512 CTGATTTTATCAGGAGCTGGCAAGTAAAGAAAGAAAGCAATCTGAAGTGAAT 571
Qy 541 GAGCTGAAGATTAAGTGTAAAGATGATCAATGAAATGGCATCCCTGTGATCC 600
Db 572 GAGCTGAAGATTAAGTGTAAAGATGATCAATGAAATGGCATCCCTGTGATCC 631
Qy 601 CTGACATGAAGG-GGGCATTTTAATGATGCTTCATG 638
Db 632 CTGACATGAAGGAGGAGCATTTAATGATGCTTCATG 670

RESULT 26
BD107926 848 bp DNA linear PAT 18-SEP-2002
LOCUS EST and encoded human protein.
DEFINITION BD107926
ACCESSION BD107926.1 GI:23202744
VERSION JP 2002010789-A/3.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
TITLE EST and encoded human protein
JOURNAL Patent: JP 2002010789-A 3 15-JAN-2002;
GENSET CORP

COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/3
PD 15-JAN-2002
PR 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EYE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC Von Heijne matrix
FH Key Location/Qualifiers
FT CDS 32..697
FT sig_peptide 32..73.
FT Location/Qualifiers
source 1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

1 AATGTTGAGCTGCTCTTTTCTGTTGACCTGCAATCATGCTGAACCTGTCTCAACAGGT 60
Db 32 AATGTTGAGCTGCTCTTTTCTGTTGACCTGCAATCATGCTGAACCTGTCTCAACAGGT 91
Qy 61 GCAGAAAATGCTTTAAAGTGAAGTATGATCAAGAGCTCTGGAGATTAAGCATAT 120
Db 92 GCAGAAAATGCTTTAAAGTGAAGTATGATCAAGAGCTCTGGAGATTAAGCATAT 151
Qy 121 GCGTGGATACCAATGAAGATACCTCTCAAGGATGATGCTTCTCAATGAAGAAA 180
Db 152 GCGTGGATACCAATGAAGATACCTCTCAAGGATGATGCTTCTCAATGAAGAAA 211
Qy 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGTTCTTAATTTGCAATTAACCCAGAG 240
Db 212 GTTCCCAACAGAGAGCAAGAAATTTCCATGTTCTTAATTTGCAATTAACCCAGAG 271

Qy 241 GTATCATTTCTGGTTTGTGTGTTACAGACCTTCAAAAAATCAACGCTTCTGCTGTGAG 300
Db 272 GTATCATTTCTGGTTTGTGTGTTACAGACCTTCAAAAAATCAACGCTTCTGCTGTGAG 331
Qy 301 GTGCAATCAGCATTAAGATGAAGCAAGACCGATCAACATAGCTCTTCTTAATGAC 360
Db 332 GTGCAATCAGCATTAAGATGAAGCAAGACCGATCAACATAGCTCTTCTTAATGAC 391
Qy 361 CAATCTGGAATTTTAAAAATCCCTTCAACACTTGACCAACCAATGACCATCTGTG 420
Db 392 CAATCTGGAATTTTAAAAATCCCTTCAACACTTGACCAACCAATGACCATCTGTG 451
Qy 421 CCATCTGGAATTTTAAATTTGTGTGATTTTGTGATCATATAGTTGCAATTTGCACTA 480
Db 452 CCATCTGGAATTTTAAATTTGTGTGATTTTGTGATCATATAGTTGCAATTTGCACTA 511
Qy 481 CTGATTTTATCAGGAGCTGGCAAGTAAAGAAAGAAAGCAATCTGAAGTGAAT 540
Db 512 CTGATTTTATCAGGAGCTGGCAAGTAAAGAAAGCAATCTGAAGTGAAT 571
Qy 541 GAGCTGAAGATTAAGTGTAAAGATGATCAATGAAATGGCATCCCTGTGATCC 600
Db 572 GAGCTGAAGATTAAGTGTAAAGATGATCAATGAAATGGCATCCCTGTGATCC 631
Qy 601 CTGACATGAAGG-GGGCATTTTAATGATGCTTCATG 638
Db 632 CTGACATGAAGGAGGAGCATTTAATGATGCTTCATG 670

RESULT 27
BD131408 848 bp DNA linear PAT 18-SEP-2002
LOCUS cDNA encoding secretory protein.
DEFINITION BD131408
ACCESSION BD131408.1 GI:23226353
VERSION JP 2002502605-A/22.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 848)
AUTHORS Bougueleret,L., Duclert,A. and Edwards,J.B.D.M.
TITLE cDNA encoding secretory protein
JOURNAL Patent: JP 2002502605-A 22 29-JAN-2002;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2002502605-A/22
PD 29-JAN-2002
PR 09-FEB-1999 JP 2000530603
PR 09-FEB-1998 US 60/074121, 13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116, 04-SEP-1998 US 60/099273 PI LYDIE
BOUGUELERET, AMERIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12M1/00, C12M1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G06F17/30, C12N15/00, PC
C12N5/00,
CC Von Heijne matrix
FH Key Location/Qualifiers
FT sig_peptide 32..73.
FT Location/Qualifiers
source 1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

1 AATGTTGAGCTGCTCTTTTCTGTTGACCTGCAATCATGCTGAACCTGTCTCAACAGGT 60

DB 32 AGTTGTGCTCTCTTTTCTGAGCTGACCTCATCTGACCTCTCAACGAGT 91
|||
QY 61 GCAGAAAATGCTTTTAAAGTGAAGCTTAGATACAGAACAGCTCTGGAGATAAGCATAT 120
|||
DB 92 GCAGAAAATGCTTTTAAAGTGAAGCTTAGATACAGAACAGCTCTGGAGATAAGCATAT 151
|||
QY 121 GCCTGGAGTACCAATGAAGATACCTCTCAAGCATGTAGCTTTCTTCATGAGAAA 180
|||
DB 152 GCCTGGAGTACCAATGAAGATACCTCTCAAGCATGTAGCTTTCTTCATGAGAAA 211
|||
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCATGCTCTACTTTGCAATGTAACTCAGAGG 240
|||
DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCATGCTCTACTTTGCAATGTAACTCAGAGG 271
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QY 241 GTATCATTTCTGTTTGTGTACAGACCTTCACAAAATACACCTCTCTGTGTAG 300
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DB 272 GTATCATTTCTGTTTGTGTACAGACCTTCACAAAATACACCTCTCTGTGTAG 331
|||
QY 301 GTGCAATCAGCCATGAAGATGAACAGAAACCGGATCAACATGCTCTCTTAATGAC 360
|||
DB 332 GTGCAATCAGCCATGAAGATGAACAGAAACCGGATCAACATGCTCTCTTAATGAC 391
|||
QY 361 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGAGCCATCTGTG 420
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DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGAGCCATCTGTG 451
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DB 452 CCATCTGATATTTATTTATTTGTGTATTTTGTATCATCATATGTGAATTTGACAT 511
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DB 512 CTGATTTTATCAGAGGATCTGCAACCTGAGAAAGAAACAAAGACATCTGAATGAT 571
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QY 541 GACGCTGAAGATTAAGTGTGAAAACATGATCAATTTGAATGCAATCCCTCTGATCCC 600
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DB 572 GACGCTGAAGATTAAGTGTGAAAACATGATCAATTTGAATGCAATCCCTCTGATCCC 631
|||
QY 601 CTGACATGAAAGG-GGGCATATTATTAATGATGCTTCATG 638
|||
DB 632 CTGACATGAAAGGAGGAGGAGCATATTATTAATGATGCTTCATG 670
|||

RESULT 28
BD139270 848 bp DNA linear PAT 18-SEP-2002
DEFINITION Extended cDNA of secretory protein.
ACCESSION BD139270
VERSION BD139270.1 GI:23234215
KEYWORDS JP 2002508182-A/22.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Bougueler, L., Duclert, A. and Edwards, J. B. D. M.
AUTHORS Extended cDNA of secretory protein
TITLE Patent: JP 2002508182-A 22 19-MAR-2002;
JOURNAL GENSET
COMMENT OS Homo sapiens (human)
PN JP 2002508182-A/22
PD 19-MAR-2002
PR 17-DEC-1998 JP 2000539136
PR 17-DEC-1997 US 60/069957, 09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELER, L., DUCLERT, A. and EDWARDS, J. B. D. M.
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
Von Heijne matrix
FH Key Location/Qualifiers
FT 818 peptide 32..73.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

Query Match 98.0%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 AGTTGTGCTCTCTTTTCTGAGCTGACCTCATCTGACCTCTCAACGAGT 60
|||
DB 32 AGTTGTGCTCTCTTTTCTGAGCTGACCTCATCTGACCTCTCAACGAGT 91
|||
QY 61 GCAGAAAATGCTTTTAAAGTGAAGCTTAGATACAGAACAGCTCTGGAGATAAGCATAT 120
|||
DB 92 GCAGAAAATGCTTTTAAAGTGAAGCTTAGATACAGAACAGCTCTGGAGATAAGCATAT 151
|||
QY 121 GCCTGGAGTACCAATGAAGATACCTCTCAAGCATGTAGCTTTCTTCATGAGAAA 180
|||
DB 152 GCCTGGAGTACCAATGAAGATACCTCTCAAGCATGTAGCTTTCTTCATGAGAAA 211
|||
QY 181 GTTCCCAACAGAGAACCAAGAAATTTCCATGCTCTACTTTGCAATGTAACTCAGAGG 240
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DB 212 GTTCCCAACAGAGAACCAAGAAATTTCCATGCTCTACTTTGCAATGTAACTCAGAGG 271
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QY 241 GTATCATTTCTGTTTGTGTACAGACCTTCACAAAATACACCTCTCTGTGTAG 300
|||
DB 272 GTATCATTTCTGTTTGTGTACAGACCTTCACAAAATACACCTCTCTGTGTAG 331
|||
QY 301 GTGCAATCAGCCATGAAGATGAACAGAAACCGGATCAACATGCTCTCTTAATGAC 360
|||
DB 332 GTGCAATCAGCCATGAAGATGAACAGAAACCGGATCAACATGCTCTCTTAATGAC 391
|||
QY 361 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGAGCCATCTGTG 420
|||
DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGAGCCATCTGTG 451
|||
QY 421 CCATCTGATATTTATTTATTTGTGTATTTTGTATCATCATATGTGAATTTGACAT 480
|||
DB 452 CCATCTGATATTTATTTATTTGTGTATTTTGTATCATCATATGTGAATTTGACAT 511
|||
QY 481 CTGATTTTATCAGAGGATCTGCAACCTGAGAAAGAAACAAAGACATCTGAATGAT 540
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DB 512 CTGATTTTATCAGAGGATCTGCAACCTGAGAAAGAAACAAAGACATCTGAATGAT 571
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QY 541 GACGCTGAAGATTAAGTGTGAAAACATGATCAATTTGAATGCAATCCCTCTGATCCC 600
|||
DB 572 GACGCTGAAGATTAAGTGTGAAAACATGATCAATTTGAATGCAATCCCTCTGATCCC 631
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QY 601 CTGACATGAAAGG-GGGCATATTATTAATGATGCTTCATG 638
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DB 632 CTGACATGAAAGGAGGAGGAGCATATTATTAATGATGCTTCATG 670
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RESULT 29
BD203799 848 bp DNA linear PAT 17-JUL-2003
DEFINITION 5'EST and human protein encoded thereby.
ACCESSION BD203799
VERSION BD203799.1 GI:33013569
KEYWORDS JP 2002511259-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE Edwards, J. B. D. M., Duclert, A. and Giordano, J. V.
AUTHORS 5'EST and human protein encoded thereby
TITLE Patent: JP 2002511259-A 3 16-APR-2002;
JOURNAL GENSET
COMMENT OS Homo sapiens (human)

PN JP 2002511259-A/3
PD 16-APR-2002
PR 09-APR-1999 JP 2000543599
PR 09-APR-1998 US 09/057719, 28-APR-1998 US 09/069047 PI
JENAN BAPTISTE DOMAS MILNE EDMARDS, AMERIC DOUGLERT, JEAN YVES PI
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12M1/00, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, C12P21/02, C12Q1/68, G01N33/53, G01N33/566, PC
G06F17/50//
PC G06F17/30, C12N15/00, C12N5/00, C12N15/00
CC Von Heljne matrix
FH Key Location/Qualifiers
FT CDS 32.. 697
FT sig peptide 32.. 73.
FT Location/Qualifiers
FEATURES
1..848
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 96.4%; Score 625; DB 6; Length 848;
Best Local Similarity 99.2%; Pred. No. 9.3e-162;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;
1 ATGTTGGCGTCTCTTTTCTGTCGACCTGACCTTCACTGACCTGTCACACAGT 60
|||
32 ATGTTGGCGTCTCTTTTCTGTCGACCTGACCTTCACTGACCTGTCACACAGT 91
|||
61 GCAGAAATGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 120
|||
92 GCAGAAATGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 151
|||
121 GCCTGGATACCAATGAAATACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAT 180
|||
152 GCCTGGATACCAATGAAATACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAT 211
|||
181 GTTCCCAAG 240
|||
212 GTTCCCAAG 271
|||
241 GTATCATTTGCTTGTGTGTACAGACCTTCAAAAAATCAACCTTCTGCTGTGAG 300
|||
272 GTATCATTTGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 331
|||
301 GTGCAATCAGCATAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
|||
332 GTGCAATCAGCATAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 391
|||
361 CAAATCTGGAATTTTAAAAATCCTTCCACATTTGACCAACCCATGAGACCTGTG 420
|||
392 CAAATCTGGAATTTTAAAAATCCTTCCACATTTGACCAACCCATGAGACCTGTG 451
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421 CCAATCTGGAATTTTAAAAATCCTTCCACATTTGACCAACCCATGAGACCTGTG 480
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452 CCAATCTGGAATTTTAAAAATCCTTCCACATTTGACCAACCCATGAGACCTGTG 511
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512 CTGATTTTATCAGGATCTGCAACCTAGAGAGAGAGAGAGAGAGAGAGAGAT 571
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541 GAGCTGGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 600
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572 GAGCTGGAATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 631
|||
601 CTGGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 638
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632 CTGGAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 670
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RESULT 30
BD135300

LOCUS BD135300 1356 bp DNA linear PAT 18-SEP-2002
DEFINITION 110 human secretory proteins.
ACCESSION BD135300
VERSION BD135300.1 GI:22320245
KEYWORDS JP 2002508167-A/51.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 (bases 1 to 1356)
Moore, P.A., Ruben, S.M., Carter, K.C., Shi, Y., Rosen, C.A.,
Soppet, D.R., Caou, H., Wei, Y.F., Florence, K., Duan, R.D.,
Florence, C., Greene, J.M., Feng, P., Ferrite, A.M., Yu, G.L., Janat, F.
and Ni, J.
110 human secretory proteins
Patent: JP 2002508167-A 51 19-MAR-2002;
HUMAN GENOME SCIENCES INC
OS Homo sapiens (human)
PN JP 2002508167-A/51
PD 19-MAR-2002
PR 17-DEC-1998 JP 2000539040
PR 18-DEC-1997 US 60/070 923, 18-DEC-1997 US 60/068 007 PR
PR 18-DEC-1997 US 60/068 057, 18-DEC-1997 US 60/068 006 PR
PR 18-DEC-1997 US 60/068 008, 18-DEC-1997 US 60/068 054 PR
PR 18-DEC-1997 US 60/068 064, 18-DEC-1997 US 60/068 053 PR
PR 19-DEC-1997 US 60/068 169, 19-DEC-1997 US 60/068 368 PR
PR 19-DEC-1997 US 60/068 367, 19-DEC-1997 US 60/068 369 PR
PR 19-DEC-1997 US 60/068 365
PI PAUL A MOORE, STEVEN M RUBEN, KENNETH C CARTER, YANGGU SHI, CRAIG
PI A ROSEN,
PI DANIEL R SOPPET, HARA CAOU, YING FEI WEI, KIMBERLY FLORENCE, PI
ROSANNE D DUAN,
PI CHARLES FLORENCE, JOHN M GREENE, PING FENG, ANN M FERRIE, GUO PI
LIANG YU,
PI FORD JANAT, JIAN NI
PC C12N15/09, A61K38/00, A61K48/00, A61P9/00, A61P9/10, A61P15/00, PC
A61P25/00,
PC A61P25/02, A61P25/14, A61P25/16, A61P25/18, A61P25/22, A61P25/24,
PC A61P25/28,
PC A61P29/00, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/10,
PC C12P21/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, C12N15/00, PC
A61K37/02,
PC C12N5/00
CC n equals a, t, g, or c
FH Key Location/Qualifiers
FT source 1..1356
FT Location/Qualifiers
1..1356
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 96.4%; Score 615; DB 6; Length 1356;
Best Local Similarity 99.7%; Pred. No. 5.4e-159;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
1 ATGTTGGCGTCTCTTTTCTGTCGACCTGACCTTCACTGACCTGTCACACAGT 60
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18 ATGTTGGCGTCTCTTTTCTGTCGACCTGACCTTCACTGACCTGTCACACAGT 77
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61 GCAGAAATGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 120
|||
78 GCAGAAATGCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 137
|||
121 GCTGGATACCAATGAAATACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAT 180
|||
138 GCTGGATACCAATGAAATACCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAT 197
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181 GTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 240
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Oy      241 GTATCATTTCTGTTGGTTGTACAGACCCCTTCAAAAATCAACCCCTTCTGCTTTGAG 300
Db      257 GTATCATTTCTGTTGGTTGTACAGACCCCTTCAAAAATCAACCCCTTCTGCTTTGAG 316
Oy      301 GTGCAATGACCATAGATAGATGAACAGAAACCGGATCAACATGCTTCTTTCTAATGAC 360
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Oy      361 CAAACTCTGAAATTTTAAAAATCCCTTCACACTTGACACACCATGGAACCATCTGTG 420
Db      377 CAAACTCTGAAATTTTAAAAATCCCTTCACACTTGACACACCATGGAACCATCTGTG 436
Oy      421 CCATCTGATTAATTAATTTGGTGTGATATTTGCAATCAATAGTGCATTTGCACTA 480
Db      437 CCATCTGATTAATTAATTTGGTGTGATATTTGCAATCAATAGTGCATTTGCACTA 496
Oy      481 CTGATTTTATCAGGGATCTGGCAAGTAGAAGAAAGAACAAAGAACATCTGAATGAT 540
Db      497 CTGATTTTATCAGGGATCTGGCAAGTAGAAGAAAGAACAAAGAACATCTGAATGAT 556
Oy      541 GAGCTGAAGATAGTGTGAAAAATGATCAACAATTGAATGCAATCCCTCTGATCCC 600
Db      557 GAGCTGAAGATAGTGTGAAAAATGATCAACAATTGAATGCAATCCCTCTGATCCC 616
Oy      601 CTGAACATGAAGGG-GGGCATATTAAATGATGCTTCATG 638
Db      617 CTGAACATGAAGGGAGGCATATTAAATGATGCTTCATG 655
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Job time : 2507.23 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 13:05:30 ; Search time 273.337 Seconds
(without alignments)
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Title: US-09-989-724-386_COPY_7_644

Perfect score: 638
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2995936 seqs, 228098010 residues

Total number of hits satisfying chosen parameters: 518

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 6500 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US04_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US03_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US01_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US04_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US03_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US01_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	638	100.0	1346	9	US-09-989-722-386 Sequence 386, App
2	638	100.0	1346	9	US-09-989-723-386 Sequence 386, App
3	638	100.0	1346	9	US-09-989-727-386 Sequence 386, App
4	638	100.0	1346	9	US-09-989-727-386 Sequence 386, App
5	638	100.0	1346	9	US-09-989-731-386 Sequence 386, App
6	638	100.0	1346	9	US-09-989-732-386 Sequence 386, App
7	638	100.0	1346	9	US-09-991-073-386 Sequence 386, App
8	638	100.0	1346	9	US-09-991-442-386 Sequence 386, App
9	638	100.0	1346	9	US-09-991-163-386 Sequence 386, App
10	638	100.0	1346	9	US-09-993-604-386 Sequence 386, App
11	638	100.0	1346	9	US-09-990-456-386 Sequence 386, App
12	638	100.0	1346	9	US-09-989-721-386 Sequence 386, App
13	638	100.0	1346	9	US-09-992-598-386 Sequence 386, App
14	638	100.0	1346	9	US-09-989-293A-386 Sequence 386, App

15	638	100.0	1346	9	US-09-989-735-386 Sequence 386, App
16	638	100.0	1346	9	US-09-990-444-386 Sequence 386, App
17	638	100.0	1346	9	US-09-991-181-386 Sequence 386, App
18	638	100.0	1346	9	US-09-989-730-386 Sequence 386, App
19	638	100.0	1346	9	US-09-990-436-386 Sequence 386, App
20	638	100.0	1346	9	US-09-993-687-386 Sequence 386, App
21	638	100.0	1346	10	US-09-989-734-386 Sequence 386, App
22	638	100.0	1346	10	US-09-997-653-386 Sequence 386, App
23	638	100.0	1346	10	US-09-993-667-386 Sequence 386, App
24	638	100.0	1346	10	US-09-997-428-386 Sequence 386, App
25	638	100.0	1346	10	US-09-997-668-386 Sequence 386, App
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83	638	100.0	1346	13	US-10-128-685A-481 Sequence 481, App
84	638	100.0	1346	13	US-10-131-820A-481 Sequence 481, App
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91	638	100.0	1346	15	US-10-121-049-481	Sequence 481, App	164	638	100.0	1346	15	US-10-127-8454-481	Sequence 481, App
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94	638	100.0	1346	15	US-10-175-746-481	Sequence 481, App	167	638	100.0	1346	15	US-10-127-8499-481	Sequence 481, App
95	638	100.0	1346	15	US-10-176-918-481	Sequence 481, App	168	638	100.0	1346	15	US-10-127-8508-481	Sequence 481, App
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113	638	100.0	1346	15	US-10-121-045-481	Sequence 481, App	186	638	100.0	1346	15	US-10-123-235-481	Sequence 481, App
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237	638	100.0	1346	15	US-10-153-934-481	Sequence 481, App	310	638	100.0	1346	15	US-10-145-091-481	Sequence 481, App
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390	638	100.0	1346	15	US-10-152-373-481	Sequence 481, App	463	638	100.0	1346	16	US-10-142-884-481	Sequence 481, App
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392	638	100.0	1346	15	US-10-121-055-481	Sequence 481, App	465	638	100.0	1346	16	US-10-143-115-481	Sequence 481, App
393	638	100.0	1346	15	US-10-121-057-481	Sequence 481, App	466	638	100.0	1346	16	US-10-144-958-481	Sequence 481, App
394	638	100.0	1346	15	US-10-121-058-481	Sequence 481, App	467	638	100.0	1346	16	US-10-144-958-481	Sequence 481, App
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398	638	100.0	1346	15	US-10-123-154-481	Sequence 481, App	471	638	100.0	1346	16	US-10-145-871-481	Sequence 481, App
399	638	100.0	1346	15	US-10-123-157-481	Sequence 481, App	472	638	100.0	1346	16	US-10-145-878-481	Sequence 481, App
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401	638	100.0	1346	15	US-10-124-814-481	Sequence 481, App	474	638	100.0	1346	16	US-10-147-489-481	Sequence 481, App
402	638	100.0	1346	15	US-10-124-816-481	Sequence 481, App	475	638	100.0	1346	16	US-10-147-507-481	Sequence 481, App
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404	638	100.0	1346	15	US-10-125-704-481	Sequence 481, App	477	638	100.0	1346	16	US-10-147-537-481	Sequence 481, App
405	638	100.0	1346	15	US-10-125-927-481	Sequence 481, App	478	638	100.0	1346	16	US-10-152-376-481	Sequence 481, App
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RESULT 1
US-09-989-722-386

ALIGNMENTS

[illegible]

DB 487 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAACAAAGACATCTGAAGTGAT 546
QY 541 GACGCTGAAGATAGTGTGAAAACATGATCAATTAAGAAATGGCATCCCTTGATCCC 600
DB 547 GACGCTGAAGATAGTGTGAAAACATGATCAATTAAGAAATGGCATCCCTTGATCCC 606
QY 601 CTGACATGAAGGGGGGCGCATATTATATGATGCGCTTCATG 638
DB 607 CTGACATGAAGGGGGGCGCATATTATATGATGCGCTTCATG 644

RESULT 508

US-10-140-927-481
; Sequence 481, Application US/10140927
; Publication No. US20040009548A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey B.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C180
; CURRENT APPLICATION NUMBER: US/10/140,927
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-927-481

Query Match 100.0%; Score 638; DB 16; Length 1346;

Best Local Similarity 100.0%; Pred. No. 2.9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTGCTGCTCTTTTCTGTGACTGCAATTCATGCTGAACCTGTCAACCAAGT 60
DB 7 ATGTTGTGCTGCTCTTTTCTGTGACTGCAATTCATGCTGAACCTGTCAACCAAGT 66
QY 61 GCAGAAAATGCTTTTAAAGTGAAGTCTAGTATGAGAAACAGCTGTGGAGATTAAGCTAT 120
DB 67 GCAGAAAATGCTTTTAAAGTGAAGTCTAGTATGAGAAACAGCTGTGGAGATTAAGCTAT 126
QY 121 GCGTGGATACCAATGAAGATACCTCTTCAAGCGATGTAGCTTTCTCATAGAAA 180
DB 127 GCGTGGATACCAATGAAGATACCTCTTCAAGCGATGTAGCTTTCTCATAGAAA 186
QY 181 GTTCCCAACAGAGAACCAAGAAATTTTCCATGTCTTACTTTGCAATGTAACCCAGAG 240
DB 187 GTTCCCAACAGAGAACCAAGAAATTTTCCATGTCTTACTTTGCAATGTAACCCAGAG 246
QY 241 GATATCTTGTGTTTGTGTTACAGACCTTCAAAAATATCAACCCCTTCTGCTGTAG 300
DB 247 GATATCTTGTGTTTGTGTTACAGACCTTCAAAAATATCAACCCCTTCTGCTGTAG 306
QY 301 GTGCAATCAGCCATGAAGATGAACAGAAACCGATCAACAATGCTTTCTTAATGAC 360

DB 307 GTGCAATCAGCCATGAAGATGAACAGAAACCGATCAACAATGCTTTCTTAATGAC 366
QY 361 CAATCTGGAATTTTAAAAATCCCTTCAACATGCAACCAACCAATCTG 420
DB 367 CAATCTGGAATTTTAAAAATCCCTTCAACATGCAACCAACCAATCTG 426
QY 421 CCATCTGATTTATTTATTTGTGTGATATTTTGCATCATATGTTGCAATTCAC 480
DB 427 CCATCTGATTTATTTATTTGTGTGATATTTTGCATCATATGTTGCAATTCAC 486
QY 481 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAACAAAGACATCTGAAGTGAT 540
DB 487 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAACAAAGACATCTGAAGTGAT 546
QY 541 GACGCTGAAGATAGTGTGAAAACATGATCAATTAAGAAATGGCATCCCTTGATCCC 600
DB 547 GACGCTGAAGATAGTGTGAAAACATGATCAATTAAGAAATGGCATCCCTTGATCCC 606
QY 601 CTGACATGAAGGGGGGCGCATATTATATGATGCGCTTCATG 638
DB 607 CTGACATGAAGGGGGGCGCATATTATATGATGCGCTTCATG 644

RESULT 509

US-10-147-536-481
; Sequence 481, Application US/10147536
; Publication No. US20040077064A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Geritsen, Mary E.
; APPLICANT: Goddard, Audrey B.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P330R1C349
; CURRENT APPLICATION NUMBER: US/10/147,536
; CURRENT FILING DATE: 2002-05-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 481
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-147-536-481

Query Match 100.0%; Score 638; DB 17; Length 1346;

Best Local Similarity 100.0%; Pred. No. 2.9e-186; Mismatches 0; Indels 0; Gaps 0;

Matches 638; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTGTGCTGCTCTTTTCTGTGACTGCAATTCATGCTGAACCTGTCAACCAAGT 60
DB 7 ATGTTGTGCTGCTCTTTTCTGTGACTGCAATTCATGCTGAACCTGTCAACCAAGT 66
QY 61 GCAGAAAATGCTTTTAAAGTGAAGTCTAGTATGAGAAACAGCTGTGGAGATTAAGCTAT 120
DB 67 GCAGAAAATGCTTTTAAAGTGAAGTCTAGTATGAGAAACAGCTGTGGAGATTAAGCTAT 126
QY 121 GCGTGGATACCAATGAAGATACCTCTTCAAGCGATGTAGCTTTCTCATAGAAA 180
DB 127 GCGTGGATACCAATGAAGATACCTCTTCAAGCGATGTAGCTTTCTCATAGAAA 186

QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGTCCTACTTGTGCAATGTAACCCAGAGG 240
DB 187 GTTCCCAACAGAGAGCAAGAAATTTCCATGTCCTACTTGTGCAATGTAACCCAGAGG 246
QY 241 GTATCATTTCTGTTTGTGTGTACAGACCCCTCAAAAAATCAACCCCTTCTGCTGTGAG 300
DB 247 GTATCATTTCTGTTTGTGTGTGTACAGACCCCTCAAAAAATCAACCCCTTCTGCTGTGAG 306
QY 301 GTGCAATCAGCCATTAAGATGAACAAGAACCGGATCAACAATGCTTTCTTAATATAC 360
DB 307 GTGCAATCAGCCATTAAGATGAACAAGAACCGGATCAACAATGCTTTCTTAATATAC 366
QY 361 CAAACTCTGAAATTTTAAAAATCCCTTCACTGTGACCAACCCATGCAATCTGTG 420
DB 367 CAAACTCTGAAATTTTAAAAATCCCTTCACTGTGACCAACCCATGCAATCTGTG 426
QY 421 CCCATCTGATTTATTAATTTGTGTGTATTTTGTGATCATCATATGTTGCAATGCACTA 480
DB 427 CCCATCTGATTTATTAATTTGTGTGTATTTTGTGATCATCATATGTTGCAATGCACTA 486
QY 481 CTGATTTTATCAGGATCTGGCAACGTGAGAAAGAAACAAGAACATCTGAAGTGAT 540
DB 487 CTGATTTTATCAGGATCTGGCAACGTGAGAAAGAAACAAGAACATCTGAAGTGAT 546
QY 541 GACGCTGAAGATTAAGTGTGAACCAATGATCAATTTGCAATGCAATGCAATGCAATGCC 600
DB 547 GACGCTGAAGATTAAGTGTGAACCAATGATCAATTTGCAATGCAATGCAATGCAATGCC 606
QY 601 CTGACATGAAGAGGGGCAATTAATGATGCTTCATG 638
DB 607 CTGACATGAAGAGGGGCAATTAATGATGCTTCATG 644

RESULT 510

US-10-133-013-205
; Sequence 205, Application US/10133013
; Publication No. US20030166903A1
; GENERAL INFORMATION:
; APPLICANT: Astromoff, Anna
; APPLICANT: Bandman, Olga
; APPLICANT: Cohen, Benjamin G.
; TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
; FILE REFERENCE: PA-0049 US
; CURRENT APPLICATION NUMBER: US/10/133,013
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/287,067
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PERL Program
; SEQ ID NO 205
; LENGTH: 1312
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 2580580CB1
US-10-133-013-205

Query Match 98.3%; Score 627; DB 15; Length 1312;
Best Local Similarity 99.8%; Pred. No. 7, 2e-183;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTTTGCGCTCTTTTCTGTGATCGCATTCATGCAATCTCTGCAACAGAT 60
DB 9 ATGTTTGCGCTCTTTTCTGTGATCGCATTCATGCAATCTCTGCAACAGAT 68
QY 61 GCAGAAATGCTTTAAAGTGAAGCTTATCAGAACAGCTCTGGAGATAAAGCATAT 120
DB 69 GCAGAAATGCTTTAAAGTGAAGCTTATCAGAACAGCTCTGGAGATAAAGCATAT 128
QY 121 GCTGGGATACCAATGAAGATACCTTTCAAGGAGATGATCTTTCTCAGTGAAGAA 180

DB 129 GCTGGGATACCAATGAAGATACCTTTCAAGGAGATGATCTTTCTCAGTGAAGAA 188
QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGTCCTACTTGTGCAATGTAACCCAGAGG 240
DB 189 GTTCCCAACAGAGAGCAAGAAATTTCCATGTCCTACTTGTGCAATGTAACCCAGAGG 248
QY 241 GTATCATTTCTGTTTGTGTGTGTACAGACCCCTCAAAAAATCAACCCCTTCTGCTGTGAG 300
DB 249 GTATCATTTCTGTTTGTGTGTGTGTACAGACCCCTCAAAAAATCAACCCCTTCTGCTGTGAG 308
QY 301 GTGCAATCAGCCATTAAGATGAACAAGAACCGGATCAACAATGCTTTCTTAATATAC 360
DB 309 GTGCAATCAGCCATTAAGATGAACAAGAACCGGATCAACAATGCTTTCTTAATATAC 368
QY 361 CAAACTCTGAAATTTTAAAAATCCCTTCACTGTGACCAACCCATGCAATCTGTG 420
DB 369 CAAACTCTGAAATTTTAAAAATCCCTTCACTGTGACCAACCCATGCAATCTGTG 428
QY 421 CCCATCTGATTTATTAATTTGTGTGTATTTTGTGATCATCATATGTTGCAATGCACTA 480
DB 429 CCCATCTGATTTATTAATTTGTGTGTATTTTGTGATCATCATATGTTGCAATGCACTA 488
QY 481 CTGATTTTATCAGGATCTGGCAACGTGAGAAAGAAACAAGAACATCTGAAGTGAT 540
DB 489 CTGATTTTATCAGGATCTGGCAACGTGAGAAAGAAACAAGAACATCTGAAGTGAT 548
QY 541 GACGCTGAAGATTAAGTGTGAACCAATGATCAATTTGCAATGCAATGCAATGCAATGCC 600
DB 549 GACGCTGAAGATTAAGTGTGAACCAATGATCAATTTGCAATGCAATGCAATGCAATGCC 608
QY 601 CTGACATGAAGAGG-GGGCAATTAATGATGCTTCATG 638
DB 609 CTGACATGAAGAGG-GGGCAATTAATGATGCTTCATG 647

RESULT 511

US-10-372-876-17
; Sequence 17, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 1432
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-372-876-17

Query Match 98.3%; Score 627; DB 13; Length 1432;
Best Local Similarity 99.8%; Pred. No. 7,6e-183;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 1 AAGTTGGCTGCTCTTTTCTGAGTCCATTCAGCTGTAACCTGTAACCAAGT 60
DB 69 AAGTTGGCTGCTCTTTTCTGAGTCCATTCAGCTGTAACCTGTAACCAAGT 128
QY 61 GCAGAAATGCTTTTAAAGTGAAGTATGATGAGAAACAGCTGGAGATTAAGCATAT 120
DB 129 GCAGAAATGCTTTTAAAGTGAAGTATGATGAGAAACAGCTGGAGATTAAGCATAT 188
QY 121 GCTGGGATACCAATGAAGATACCTCTTCAAGGCAATGGTACCTTCTCATGAGAAA 180
DB 189 GCTGGGATACCAATGAAGATACCTCTTCAAGGCAATGGTACCTTCTCATGAGAAA 248
QY 181 GTTCCCAACAGAGAACACAGAAATTTCCATGCTTACTTTGCAATGTAACCCAGAG 240
DB 249 GTTCCCAACAGAGAACACAGAAATTTCCATGCTTACTTTGCAATGTAACCCAGAG 308
QY 241 GATATCATTCGTTTGGTTTGAAGACCCCTTCAAAAATACACCCCTTCTGCTGTTAG 300
DB 309 GATATCATTCGTTTGGTTTGAAGACCCCTTCAAAAATACACCCCTTCTGCTGTTAG 368
QY 301 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTTCTTCTTAATGAC 360
DB 369 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTTCTTCTTAATGAC 428
QY 361 CAACTCTGGAATTTTAAATATCCCTTCCACACTTGCAACCCCATGAGCCCATGTG 420
DB 429 CAACTCTGGAATTTTAAATATCCCTTCCACACTTGCAACCCCATGAGCCCATGTG 488
QY 421 CCCATCTGATATTAATATTTGGTGAATTTTGTGATCATCATGATGCAATTTGACATA 480
DB 489 CCCATCTGATATTAATATTTGGTGAATTTTGTGATCATCATGATGCAATTTGACATA 548
QY 481 CTGATTTTATCAGGATCTGGCAACGTAGAAAGAAAGAAAGAACCATCTGAAGTGAT 540
DB 549 CTGATTTTATCAGGATCTGGCAACGTAGAAAGAAAGAAAGAACCATCTGAAGTGAT 608
QY 541 GAGCTGAAGATTAAGTGTGAAGACATGATCAATGAAGAAATGSCATCCCTCTGATCCC 600
DB 609 GAGCTGAAGATTAAGTGTGAAGACATGATCAATGAAGAAATGSCATCCCTCTGATCCC 668
QY 601 CTGACATGAAGGG-GGGCATATTATGATGCTTCATG 638
DB 669 CTGACATGAAGGGAGGGCATATTATGATGCTTCATG 707
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RESULT 512
US-10-097-065-17
; Sequence 17, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: PZ021P1
; CURRENT APPLICATION NUMBER: US/10/097, 065
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070, 923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068, 007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068, 057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068, 006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068, 369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068, 367

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; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: 60/068,368  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: 60/068,169  
; PRIOR FILING DATE: 1997-12-19  
; PRIOR APPLICATION NUMBER: 60/068,053  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,064  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,054  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,008  
; PRIOR FILING DATE: 1997-12-18  
; PRIOR APPLICATION NUMBER: 60/068,365  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 1432  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-097-065-17
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Query Match 98.3%; Score 627; DB 15; Length 1432;
Best Local Similarity 99.8%; Pred. No. 7,6e-183;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
QY 1 AAGTTGGCTGCTCTTTTCTGAGTCCATTCAGCTGTAACCTGTAACCAAGT 60
DB 69 AAGTTGGCTGCTCTTTTCTGAGTCCATTCAGCTGTAACCTGTAACCAAGT 128
QY 61 GCAGAAATGCTTTTAAAGTGAAGTATGATGAGAAACAGCTGGAGATTAAGCATAT 120
DB 129 GCAGAAATGCTTTTAAAGTGAAGTATGATGAGAAACAGCTGGAGATTAAGCATAT 188
QY 121 GCTGGGATACCAATGAAGATACCTCTTCAAGGCAATGGTACCTTCTCATGAGAAA 180
DB 189 GCTGGGATACCAATGAAGATACCTCTTCAAGGCAATGGTACCTTCTCATGAGAAA 248
QY 181 GTTCCCAACAGAGAACACAGAAATTTCCATGCTTACTTTGCAATGTAACCCAGAG 240
DB 249 GTTCCCAACAGAGAACACAGAAATTTCCATGCTTACTTTGCAATGTAACCCAGAG 308
QY 241 GATATCATTCGTTTGGTTTGAAGACCCCTTCAAAAATACACCCCTTCTGCTGTTAG 300
DB 309 GATATCATTCGTTTGGTTTGAAGACCCCTTCAAAAATACACCCCTTCTGCTGTTAG 368
QY 301 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTTCTTCTTAATGAC 360
DB 369 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTTCTTCTTAATGAC 428
QY 361 CAACTCTGGAATTTTAAATATCCCTTCCACACTTGCAACCCCATGAGCCCATGTG 420
DB 429 CAACTCTGGAATTTTAAATATCCCTTCCACACTTGCAACCCCATGAGCCCATGTG 488
QY 421 CCCATCTGATATTAATATTTGGTGAATTTTGTGATCATCATGATGCAATTTGACATA 480
DB 489 CCCATCTGATATTAATATTTGGTGAATTTTGTGATCATCATGATGCAATTTGACATA 548
QY 481 CTGATTTTATCAGGATCTGGCAACGTAGAAAGAAAGAAAGAACCATCTGAAGTGAT 540
DB 549 CTGATTTTATCAGGATCTGGCAACGTAGAAAGAAAGAAAGAACCATCTGAAGTGAT 608
QY 541 GAGCTGAAGATTAAGTGTGAAGACATGATCAATGAAGAAATGSCATCCCTCTGATCCC 600
DB 609 GAGCTGAAGATTAAGTGTGAAGACATGATCAATGAAGAAATGSCATCCCTCTGATCCC 668
QY 601 CTGACATGAAGGG-GGGCATATTATGATGCTTCATG 638
DB 669 CTGACATGAAGGGAGGGCATATTATGATGCTTCATG 707
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RESULT 513

Db 377 GTGCAATGACCCATTAAGATGAACAAGACCGGATCAACATGCTCTTTCTTAATGAC 436
Qy 361 CAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGGAATCCATCTGAG 420
Db 437 CAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGGAATCCATCTGAG 496
Qy 421 CCCATCTGATATATATATTTGGTGTGATATTTTGATCATATAGTTGCAATGACACTA 480
Db 497 CCCATCTGATATATATATTTGGTGTGATATTTTGATCATATAGTTGCAATGACACTA 556
Qy 481 CTGATTTTATCAGGAGTCTGGCAACGTAGAGAAAGAACCAAGACCATCTGAAGTGAT 540
Db 557 CTGATTTTATCAGGAGTCTGGCAACGTAGAGAAAGAACCAAGACCATCTGAAGTGAT 616
Qy 541 GACGCTGAAGATTAAGTGTGAAAAATCATGATCAATTTGAATAGCATCCCTCTGATCCC 600
Db 617 GACGCTGAAGATTAAGTGTGAAAAATCATGATCAATTTGAATAGCATCCCTCTGATCCC 676
Qy 601 CTGACATGAAGAGG-GGGCATATTATGATGCTTCATG 638
Db 677 CTGACATGAAGAGGAGGGCATATTATGATGCTTCATG 715

RESULT 515

US-09-903-190-27
Sequence 27, Application US/09903190
Publication No. US20030162176A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleit, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT APPLICATION NUMBER: US/09/903,190
PRIOR FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/247,155A
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 27
LENGTH: 848
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 32..73
OTHER INFORMATION: Von Heijne matrix
US-09-903-190-27

Query Match 98.0%; Score 625; DB 10; Length 848;

Best Local Similarity 99.2%; Pred. No. 2.3e-182;

Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

Qy 1 ATGTTGTGCTGCTCTTTTTCGTGACATGCAATTCAGCTGCAACTCTGTCAACAGGT 60
Db 32 ATGTTGTGCTGCTCTTTTTCGTGACATGCAATTCAGCTGCAACTCTGTCAACAGGT 91
Qy 61 GGAGAAAAAGCTTTTAAAGTGAAGACTTATGATCAGAACAGCTCTGGAGATAAGCATAT 120
Db 92 GGAGAAAAAGCTTTTAAAGTGAAGACTTATGATCAGAACAGCTCTGGAGATAAGCATAT 151
Qy 121 GCCTGGATACCAATGAAGATACCTCTTCAAGCAAGGTAGCTTTCTCCATGAGAAA 180
Db 152 GCCTGGATACCAATGAAGATACCTCTTCAAGCAAGGTAGCTTTCTCCATGAGAAA 211

Qy 181 GTTCCCAAGAGAGCAAGCAAGAAATTTCCATGCTCTTGTCAATGTAACCAAGAG 240
Db 212 GTTCCCAAGAGAGCAAGCAAGAAATTTCCATGCTCTTGTCAATGTAACCAAGAG 271
Qy 241 GATATCTTCTGTTGTGTGTTACAGACCTTCAAAAAATACACCTTCTGCTGTAG 300
Db 272 GATATCTTCTGTTGTGTGTTACAGACCTTCAAAAAATACACCTTCTGCTGTAG 331
Qy 301 GTGCAATCAGCCATTAAGATGAACAAGAACCGGATCAACAAATGCTCTTCTAAATGAC 360
Db 332 GTGCAATCAGCCATTAAGATGAACAAGAACCGGATCAACAAATGCTCTTCTAAATGAC 391
Qy 361 CAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGGAATCCATCTGAG 420
Db 392 CAACTCTGGAATTTTAAATAATCCCTTCACACTTGACACCCATGGAATCCATCTGAG 451
Qy 421 CCCATCTGATATATATATTTGGTGTGATATTTTGATCATATAGTTGCAATGACACTA 480
Db 452 CCCATCTGATATATATATTTGGTGTGATATTTTGATCATATAGTTGCAATGACACTA 511
Qy 481 CTGATTTTATCAGGAGTCTGGCAACGTAGAGAAAGAACCAAGACCATCTGAAGTGAT 540
Db 512 CTGATTTTATCAGGAGTCTGGCAACGTAGAGAAAGAACCAAGACCATCTGAAGTGAT 571
Qy 541 GACGCTGAAGATTAAGTGTGAAAAATCATGATCAATTTGAATAGCATCCCTCTGATCCC 600
Db 572 GACGCTGAAGATTAAGTGTGAAAAATCATGATCAATTTGAATAGCATCCCTCTGATCCC 631
Qy 601 CTGACATGAAGAGG-GGGCATATTATGATGCTTCATG 638
Db 632 CTGACATGAAGAGGAGGGCATATTATGATGCTTCATG 670

RESULT 516

US-10-319-763-27
Sequence 27, Application US/10319763
Publication No. US20030144490A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleit, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
PRIOR FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 27
LENGTH: 848
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 32..73
OTHER INFORMATION: Von Heijne matrix
US-10-319-763-27

Query Match 98.0%; Score 625; DB 15; Length 848;

Best Local Similarity 99.2%; Pred. No. 2.3e-182;

Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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QY 1 ANGTGAGCTGCTCTTTTCTGAGTGCATTCATGCTGAACCTGCAACAGGT 60
DB 32 ANGTGAGCTGCTCTTTTCTGAGTGCATTCATGCTGAACCTGCAACAGGT 91
QY 61 GCAGAAAATGCTTTTAAAGTGAAGTACTGATCAGAACGCTCTGGAGATAAGCATAT 120
DB 92 GCAGAAAATGCTTTTAAAGTGAAGTACTGATCAGAACGCTCTGGAGATAAGCATAT 151
QY 121 GCTGGGATACCAATGAAGAAATACCTCTTCAAAAGGATGTGCTTTCTCCATGAGAAA 180
DB 152 GCTGGGATACCAATGAAGAAATACCTCTTCAAAAGGATGTGCTTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAACCAAGAAATTCCTGCTCTTCTGCAATGTAAACAGAG 240
DB 212 GTTCCCAACAGAGAACCAAGAAATTCCTGCTCTTCTGCAATGTAAACAGAG 271
QY 241 GTATCATTCGTGTTTGTGTTACAGACCTTCAGAAAATCAGACCTTCCTGTTGAG 300
DB 272 GTATCATTCGTGTTTGTGTTACAGACCTTCAGAAAATCAGACCTTCCTGTTGAG 331
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DB 332 GTGCATCAGCCATTAAGAAATGAACAGAACCCGATCACAATGCTCTTTCTAAATGAC 391
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DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCACACTGCAACCCATGAGCCATCTGTG 451
QY 421 CCCATCTGGAATTTATATTTTGTGATGATTTTGTGATCATATGTTGCAATTGCACTA 480
DB 452 CCCATCTGGAATTTATATTTTGTGATGATTTTGTGATCATATGTTGCAATTGCACTA 511
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DB 512 CTGATTTTATCGGAGATCTGCGACGTAAAGAAAGAAACCAATCTGAAGTAT 571
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RESULT 517
US-10-372-876-122
; Sequence 122, Application US/10372876
; Publication No. US20030204071A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/372,876
; CURRENT FILING DATE: 2003-02-26
; PRIOR APPLICATION NUMBER: 09/334,595
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: PCT/US98/27059
; PRIOR FILING DATE: 1998-12-17
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,007
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,057
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,006
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,369
; PRIOR FILING DATE: 1997-12-19
; PRIOR APPLICATION NUMBER: 60/068,367
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; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
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; PRIOR APPLICATION NUMBER: 60/068,169
; PRIOR FILING DATE: 1997-12-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patencin Ver. 2.0
; SEQ ID NO 122
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1231)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-372-876-122

Query Match          96.4%; Score 615; DB 13; Length 1356;
Best Local Similarity 99.7%; Pred. No. 3,8e-179;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 61 GCAGAAAATGCTTTTAAAGTGAAGTACTGATCAGAACGCTCTGGAGATAAGCATAT 120
DB 78 GCAGAAAATGCTTTTAAAGTGAAGTACTGATCAGAACGCTCTGGAGATAAGCATAT 137
QY 121 GCTGGGATACCAATGAAGAAATACCTCTTCAAAAGGATGTGCTTTCTCCATGAGAAA 180
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QY 481 CTGATTTTATCGGAGATCTGCGACGTAAAGAAAGAAACCAATCTGAAGTAT 540
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QY 541 GACGCTGAAGATTAAGTGAAGAAATCATGATCAATTTGAAATGCGCTCTGATCCC 600
DB 557 GACGCTGAAGATTAAGTGAAGAAATCATGATCAATTTGAAATGCGCTCTGATCCC 616
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RESULT 518
US-10-097-065-122
; Sequence 122, Application US/10097065
; Publication No. US20030055236A1
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A. et al.
; TITLE OF INVENTION: 110 Human Secreted Proteins
; FILE REFERENCE: P2021P1
; CURRENT APPLICATION NUMBER: US/10/097,065
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;; CURRENT FILING DATE: 2002-03-14
;; PRIOR APPLICATION NUMBER: PCT/US98/27059
;; PRIOR FILING DATE: 1998-12-17
;; PRIOR APPLICATION NUMBER: 60/070,923
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,007
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,057
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,006
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,369
;; PRIOR FILING DATE: 1997-12-19
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;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,064
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,054
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,008
;; PRIOR FILING DATE: 1997-12-18
;; PRIOR APPLICATION NUMBER: 60/068,365
;; PRIOR FILING DATE: 1997-12-19
;; NUMBER OF SEQ ID NOS: 672
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 122
;; LENGTH: 1356
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: SITE
;; LOCATION: (1231)
;; OTHER INFORMATION: n equals a,c,g, or c
US-10-097-065-122

Query Match 96.4%; Score 615; DB 15; Length 1356;
Best Local Similarity 99.7%; Pred. No. 3.8e-179;
Matches 637; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1 ATGTTGAGCTGCTCTTTTCTGTTGAGTCCATTCATGCTGAACCTCTGTCAACGAGT 60
DB 18 ATGTTGAGCTGCTCTTTTCTGTTGAGTCCATTCATGCTGAACCTCTGTCAACGAGT 77
QY 61 GCAGAAAATGCTTTAAGTGAAGCTTAGTACAGACGCTGAGAGATTAAGCATAT 120
DB 78 GCAGAAAATGCTTTAAGTGAAGCTTAGTACAGACGCTGAGAGATTAAGCATAT 137
QY 121 GCTTGGATACCAATGAAGATACCTTCAAGCGATGTAGCTTCTCCATGAGAAA 180
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QY 181 GTTCCACAGAGAGACAGAAATTTCCCATGCTTCACTTTGCAATGTAACCGAGG 240
DB 198 GTTCCACAGAGAGACAGAAATTTCCCATGCTTCACTTTGCAATGTAACCGAGG 256
QY 241 GTATCATTCGTTGTGTTAAGACCTTCAAAATAATGCAACCTTCCGCTGTGAG 300
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QY 301 GTGCAATCAGCCATGAAGATGAACAAGACCGATCAACAATGCTTCTTAATGAC 360
DB 317 GTGCAATCAGCCATGAAGATGAACAAGACCGATCAACAATGCTTCTTAATGAC 376
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DB 377 CAAACTCTGGAATTTTAAATCCCTTCAACTGACCAACCATGAGCCCATCTGTG 436

QY 421 CCATCTGATTAATTAATTTGTTGATTAATTTGCAATCATAGTTGCAATGCACTA 480
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QY 481 CTGATTTATCAGGATCTGGCAACCTGAGAAAGAAACCAATCTGAAGTGAAT 540
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QY 541 GAGCTGAAGATTAAGTGAAGAAACATGATCAATGAAATGSCATCCCTGATCC 600
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QY 601 CTGACATGAAGG-GGGCAATTAATGAATGCTTCAATG 638
DB 617 CTGACATGAAGGAGGCAATTAATGAATGCTTCAATG 655

Search completed: June 6, 2004, 16:42:32
Job time : 346.337 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: June 6, 2004, 10:39:20 ; Search time 1611.72 Seconds

(without alignments)
11820.943 Million cell updates/sec

Title: US-09-989-724-386_COPY_7_644

Perfect score: 638
Sequence: 1 atgttgctgctgctctctt.....ataatgatgctctcatg 638

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 26

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 80%

Maximum Match 100%

Listing first 65000 summaries

Database :
1: EST:
2: em_estdb:
3: em_estin:
4: em_estun:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estcom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vrt:
21: em_gss_fun:
22: em_gss_man:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rtd:
26: em_gss_pbg:
27: em_gss_vrl:
28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	623	97.6	870	12	BT760941 603043142
3	622.4	97.6	792	12	BG400845 602464068
4	619.4	97.1	663	14	CB139945 K-EST0193

5	609	95.5	639	14	CB137859	CB137859 K-EST0190
6	605.2	94.9	866	12	BG429618	BG429618 602501304
7	604	94.7	855	12	BG427247	BG427247 602494304
8	599.8	94.0	804	12	BG429705	BG429705 602493709
9	598	93.7	780	12	BG429174	BG429174 602498032
10	593	92.9	791	12	BG400319	BG400319 602464526
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12	586	91.8	808	12	BG399473	BG399473 602441206
13	585.8	91.8	736	12	BG399402	BG399402 602501161
14	584.8	91.7	859	12	BG427839	BG427839 602501524
15	584.4	91.6	677	12	BG437745	BG427745 602497114
16	584.4	91.6	782	12	BG433974	BG433974 602497374
17	580.2	90.9	978	12	BT762437	BT762437 603048828
18	577	90.4	607	14	CB125058	CB125058 K-EST0173
19	576	90.3	888	12	BG400513	BG400513 602464748
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21	562	88.1	678	12	BG429011	BG429011 602501924
22	549	86.1	602	12	BG432624	BG432624 602500789
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ALIGNMENTS

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DEFINITION Homo sapiens HCM0290 gene, VIRUTAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION AY399636
VERSION AY399636.1 GI:39755625
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 669)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Clevello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity 99.8%; Pred. No. 1.6e-163;
Matches 638; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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VERSION BG400845.1 GI:13294293
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 792)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaabs-remail.nih.gov
 Tissue Procurement: CLONTECH Laboratories, Inc.
 cDNA Library Preparation: CLONTECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
 Plate: LNCM1330 row: 9 column: 17
 High quality sequence stop: 784.
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 /note="Organ: Kidney; Vector: pDNR-LIB (Clontech); site: 1; SfiI (ggcgctcgcc); site 2: SfiI (ggcgctcgcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGCGCATTAAGGCG-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCGAGCGCGCGCATAG-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

ORIGIN
 Query Match 97.6%; Score 622.4; DB 12; Length 792;
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 DB 572 GAGCTGAGATATAGTGTGAAAACATGATCAGATTGAAAATGGCATCCCTCTGATCCC 631
 QY 601 CTGACATGAGG--GSCATTTATATGCTTCAT 637
 DB 632 CTGACATGAGGAGGAGCGCCATATATATGATGCTTCAT 671

RESULT 4
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 5', mRNA sequence.
 ACCESSION CBI39945
 VERSION CBI39945.1 GI:28113403
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 663)
 Kim, M.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R., Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and Kim, Y.S.
 21C Frontiers Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.krdb.re.kr
 Plate: 5 row: H column: 10
 High quality sequence stop: 663.
 Location/Qualifiers
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 /note="Organ: Liver; Vector: pCNS-D2; Site 1: BclRI; Site 2: NotI. The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deprotected with tobacco acid pyrophosphatase (TAP). The deprotected intact mRNA was ligated with DNA-RNA linker including BclRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of BclRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA

library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(drl)4 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10[®] with electroporation method."

ORIGIN

Query Match 97.1%; Score 619.4; DB 14; Length 663;
Best Local Similarity 99.7%; Pred. No. 2.1e-161;
Matches 631; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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DB 631 CTGACATGAAAGAGGATTAATGATGCC 663

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RESULT 5

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LOCUS K-BS190636 L4SN0368s1 Homo sapiens cDNA clone L4SN0368s1-11-F08
DEFINITION 5' mRNA sequence.

ACCESSION CB137859
VERSION CB137859.1 GI:28108763
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsaung@mail.krdb.re.kr
Plate: 11 row: P column: 08
High quality sequence stop: 639.
Location/Qualifiers

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/note="Organ: Liver; Vector: pcns-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then dephosphorylated with tabacco acid pyrophosphatase (TAP). The dephosphorylated RNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10[®] by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(drl)4 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10[®] with electroporation method."

ORIGIN

Query Match 95.5%; Score 609; DB 14; Length 639;
Best Local Similarity 100.0%; Pred. No. 1.7e-158;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTTGGGCTGCTCTTTTCTGAGTGCATTCATGCTGAACTGTCACCAAGT 60
DB 31 ATGTTGGGCTGCTCTTTTCTGAGTGCATTCATGCTGAACTGTCACCAAGT 90
QY 61 GCAGAAAATGCTTTAAAGTGAAGTCTTGAATCAAGACGCTTGGAGATAAGCATAT 120
DB 91 GCAGAAAATGCTTTAAAGTGAAGTCTTGAATCAAGACGCTTGGAGATAAGCATAT 150
QY 121 GCTTGGGATACCAATGAAGTACTCTTCAAGGATGAGTCTTCTCCATGAGAAA 180

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D	b		151 GCGTGGGATACCATGAAGAACTACTTTCCAAAAGCAATGTACATTTCCTTAGAAGAAAA 	210
Oy		181 GTGCCAACAGAAGACAAGAAATTTCCCAGTGCTACTTCTTAATGTAAACCAGAG 	240	
D	b	211 GTTCCCAAACAGAAAGCAACAGAAATTTCCAGTGCTACTTGTGAATGCACAGAG 	270	
Oy		241 GTAACATCTCCTTTGSGTTACAGACCCCTCAAAAAAAAAACAACCTTCGCGTTGAG 	300	
D	b	271 GTATCAATCTGGTTTTGTGTACACACCTTCAAAAAATCACACCTTCTGCTGTGAG 	330	
Oy		301 GTGCAATCAGCCATAAGATGAAACAAGAACCGGATCAATATGCCCTTTCTAAATGAC 	360	
D	b	331 GTGCATATCAGCCATAAGATGAAACAAGAACCGGATCAATATGCCCTTTCTAAATGAC 	390	
Oy		361 CAAACTCTGGAATTTTAAAAATCCCCCTTCCACATTGCAACCACTGAGACCATCTGTG 	420	
D	b	391 CAAACTCTGGAATTTTAAAAATCCCCCTTCCACATTGCAACCACTGAGACCATCTGTG 	450	
Oy		421 CCACATCGGATTAATAATATTTGGTGATATTTTGACATCATCATATGTGAATGACATA 	480	
D	b	451 CCCATCTGGATTAATAATATTTGGTGATATTTTGACATCATCATATGTGAATGACATA 	510	
Oy		481 CTGATTTATACAGGATCTGGCAACGTAGAAAGAAAAACAAGAACCATCTGAATGTGAT 	540	
D	b	511 CTGATTTATACAGGATCTGGCAACGTAGAAAGAAAAACAAGAACCATCTGAATGTGAT 	570	
Oy		541 GAACCTGAAGATTAAGTGTGAAAACATGATCACATTTGAAAATGGCATTCCTCTGATGCC 	600	
D	b	571 GACCTGAAGATTAAGTGTGAAAACATGATCACATTTGAAAATGGCATTCCTCTGATGCC 	630	
Oy		601 CTGGACATG 609 		
D	b	631 CTGGACATG 639 		

RESULT 6 BG429618 866 bp mRNA linear EST 14-MAR-2001

LOCUS B6250130421 NIH_MGC_75 Homo sapiens CDNA clone IMAGEI:4614937 5' ,

DEFINITION mRNA sequence.

ACCESSION BG429618

VERSION BG429618.1 GI:13336124

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Buhalypota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
Mammalia; Butleria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 866)
NIH-MGC http://mgs.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cga@bs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA library Arrayed by: The I.M.A.G.E.B. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E.B. Consortium/LMNL at:
<http://image.lnl.gov>
Plate: LCM1367 row: g column: 02
High quality sequence stopper: 707.
Location/Qualifiers
1..866

3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATATGCGC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGAGCGCGCCGACAT-gt-dr3(30)BN-3' (where B = A, C, G, or T). Average insert size = 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match	94.9%	Score 605.2	DB 12	Length 866
Best Local Similarity	99.1%	Pred. No. 2e-157		
Matches 630	Conservative 0	Mismatches 3	Indels 3	Gaps 2
QY	5	TGAGCTGCTCTTTTCTGGTGA	CTGCATTCATGCTGAACTCTGTCAACCAAGTGCAG	64
DB	35	TGAGCTGCTCTTTTCTGGTGA	CTGCATTCATGCTGAACTCTGTCAACCAAGTGCAG	94
QY	65	AAATGCTTTTAAAGTGA	CTTAGTATCAAGAGCTGTGGAGATTAACATATGCT	124
DB	95	AAATGCTTTTAAAGTGA	CTTAGTATCAAGAGCTGTGGAGATTAACATATGCT	154
QY	125	GGATATCAATGAAGATAT	CCCTTCTCAAAGGATGTAGCTTTCTCCATGAGAAAAGTTC	184
DB	155	GGATATCAATGAAGATAT	CCCTTCTCAAAGGATGTAGCTTTCTCCATGAGAAAAGTTC	214
QY	185	CCAAAGAGAGCAACAAAT	TTCCATGCTCTACTTGTCAATGTAAACCAAGAGGTAT	244
DB	215	CCAAAGAGAGCAACAAAT	TTCCATGCTCTACTTGTCAATGTAAACCAAGAGGTAT	274
QY	245	CATCTGTGTTGTGTATCA	AGCCCTTCAAAAATCAACCCCTTCGTGTGTAGATGC	304
DB	275	CATCTGTGTTGTGTATCA	AGCCCTTCAAAAATCAACCCCTTCGTGTGTAGATGC	334
QY	305	AATCAGCATATAGATGA	CAAGAACGGATCAACATGCTTCTTCTTAATGACCAA	364
DB	335	AATCAGCATATAGATGA	CAAGAACGGATCAACATGCTTCTTCTTAATGACCAA	394
QY	365	CTCTGGAATTTTAAAAAT	CCCTTCAACATCTTGACCAACCCATCTGTGCCA	424
DB	395	CTCTGGAATTTTAAAAAT	CCCTTCAACATCTTGACCAACCCATCTGTGCCA	454
QY	425	TCGTGATTTATATTTGG	TGTATTTTGCATCATATAGTTGCAATTGCACTACAGA	484
DB	455	TCGTGATTTATATTTGG	TGTATTTTGCATCATATAGTTGCAATTGCACTACAGA	514
QY	485	TTTATATCAGGATCTG	GCAAGTGAAGAACCAAGAACCATCTGAATGATGACG	544
DB	515	TTTATATCAGGATCTG	GCAAGTGAAGAACCAAGAACCATCTGAATGATGACG	574
QY	545	CTGAAGATTAAGTGA	AAAAATCATATGTAATAATGATCCCTCTGATCCCTGG	604
DB	575	CTGAAGATTAAGTGA	AAAAATCATATGTAATAATGATCCCTCTGATCCCTGG	633
QY	605	ACATGAAGG--GGCAT	TTAATGATGCTTCAG	638
DB	634	ACATGAAGG--GGCAT	TTAATGATGCTTCAG	669
RESULT 7				
LOCUS	BG427247	855 bp	mRNA	linear
DEFINITION	BG427247	855 bp	mRNA	linear
ACCESSION	BG427247	855 bp	mRNA	linear
VERSION	BG427247.1	GI:13333753		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
	1 (bases 1 to 855)			
	NIH-MGC http://mgc.ncbi.nlm.nih.gov/			

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: c9abbs-remail.nih.gov
Tissue Procurement: CLOMTECH Laboratories, Inc.
cDNA Library Preparation: CLOMTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM1349 row: h column: 01
High quality sequence stop: 735.
Location/Qualifiers

FEATURES
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1..855
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4608048"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI (ggccatcagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.7%; Score 604; DB 12; Length 855;
Best Local Similarity 99.5%; Pred. No. 4.3e-157;
Matches 637; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

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1  ATGTTGTGCTGCTCTTTTCTGTGAGTGCATTCAGTGAATCTGTCAACAGGT 60
33  ATGTTGTGCTGCTCTTTTCTGTGAGTGCATTCAGTGAATCTGTCAACAGGT 92
61  GCAGAAATGCTTTAAAGTGAAGTCTAGTATCAGAACAGCTCTGGAGATTAAGCAT 120
93  GCAGAAATGCTTTAAAGTGAAGTCTAGTATCAGAACAGCTCTGGAGATTAAGCAT 152
121  GCTTGGATACCAATGAAGATACCTCTTCAAAAGCGATGAGCTTCTCCATGAGAAA 180
153  GCTTGGATACCAATGAAGATACCTCTTCAAAAGCGATGAGCTTCTCCATGAGAAA 212
181  GTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
213  GTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 272
241  GTATCATCTGTGTTGTGTGTTACAGACCTTCAAAAATCAGACCTTCTGTGTTGAG 300
273  GTATCATCTGTGTTGTGTGTTACAGACCTTCAAAAATCAGACCTTCTGTGTTGAG 332
301  GTGCAATGAGCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
333  GTGCAATGAGCATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 392
361  CAATCTGTGAAATTTTAAATCCCTTCCAGCTTGCACCAACCAATGAGAGAGAG 420
393  CAATCTGTGAAATTTTAAATCCCTTCCAGCTTGCACCAACCAATGAGAGAGAG 452
421  CCATCTGTGAAATTTTAAATCCCTTCCAGCTTGCACCAACCAATGAGAGAGAG 480
453  CCATCTGTGAAATTTTAAATCCCTTCCAGCTTGCACCAACCAATGAGAGAGAG 512
481  CTGATTTATCAAGGATCTGGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 539
513  CTGATTTATCAAGGATCTGGCAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 572

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QY 540 TCACCTGAAGATAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 599
DB 573 TCACCTGAAGATAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 631
QY 600 CCTGACATGAAGAGG-GGGCATATTAAAGATGCTTCATG 638
DB 632 CCTGACATGAAGAGGAGGAGCATATTAAATGATCCTTCATG 671

RESULT 8
BG429705 804 bp mRNA linear EST 14-MAR-2001
LOCUS 602493709P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4607499 5',
DEFINITION mRNA sequence.
ACCESSION BG429705.1 GI:13336211
VERSION BG429705
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strauberg, Ph.D.
Email: c9abbs-remail.nih.gov
Tissue Procurement: CLOMTECH Laboratories, Inc.
cDNA Library Preparation: CLOMTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LNCM1348 row: a column: 04
High quality sequence stop: 731.
Location/Qualifiers

FEATURES

source

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/organism="Homo sapiens"
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/clone="IMAGE:4607499"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgccctcgcc); Site 2: SfiI (ggccatcagcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAAGGCGCATTAAGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCCGACATG-dT(30)BN-3' (where B = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 94.0%; Score 599.8; DB 12; Length 804;
Best Local Similarity 97.2%; Pred. No. 6.3e-156;
Matches 621; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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1  ATGTTGTGCTGCTCTTTTCTGTGAGTGCATTCAGTGAATCTGTCAACAGGT 60
32  ATGTTGTGCTGCTCTTTTCTGTGAGTGCATTCAGTGAATCTGTCAACAGGT 91
61  GCAGAAATGCTTTAAAGTGAAGTCTAGTATCAGAACAGCTCTGGAGATTAAGCAT 120
92  GCAGAAATGCTTTAAAGTGAAGTCTAGTATCAGAACAGCTCTGGAGATTAAGCAT 151
121  GCTTGGATACCAATGAAGATACCTCTTCAAAAGCGATGAGCTTCTCCATGAGAAA 180
152  GCTTGGATACCAATGAAGATACCTCTTCAAAAGCGATGAGCTTCTCCATGAGAAA 211
181  GTTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240

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Db      212 GTTCCCAACAGGAAGCAACAGAAATTTCCATGTCCTTCTTGCAATGTAACCCAGAG 271
Qy      241 GATCATTTCTGTTGGTTGCTACAGACCCCTTCAAAAATACACACCCCTGCTGTTGAG 300
Db      272 GTATCATTTCTGTTGGTTGCTACAGACCCCTTCAAAAATACACACCCCTGCTGTTGAG 331
Qy      301 GTGCATCAGCCATAGAAATGAACAGAAACCGATCAACATGCTCTTCTTAAATGAC 360
Db      332 GTGCATCAGCCATAGAAATGAACAGAAACCGATCAACATGCTCTTCTTAAATGAC 391
Qy      361 CAACTCTGGAATTTTAAATAATCCCTTCAACCTTGCAACCCATGAGCCATCTG 420
Db      392 CAACTCTGGAATTTTAAATAATCCCTTCAACCTTGCAACCCATGAGCCATCTG 451
Qy      421 CCCATCTGATATATATATTTGGTATTTTGGATTCATCATATGCAATTCAGCTA 480
Db      452 CCCATCTGATATATATATTTGGTATTTTGGATTCATCATATGCAATTCAGCTA 511
Qy      481 CTGATTTTATCAGGATCTGCAACCTAGAG-AAAGAACAAAGAACATCTGAATGGA 539
Db      512 CTGATTTTATCAGGATCTGCAACCTAGAGAACAAAGAACATCTGAATGGA 571
Qy      540 TGACGCTGAAGATTAAGTGAACATGATCACAATGGAATGCAATCCCTGATCC 589
Db      572 TGACGCTGAAGATTAAGTGAACATGATCACAATGGAATGCAATCCCTGATCC 631
Qy      600 CCGTGAACATGAAGGGGGGATATTAATGATGCTTCATG 638
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RESULT 9
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DEFINITION
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mRNA sequence.
ACCESSION
BG429174
VERSION
BG429174.1 GI:13335680
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 780)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM1359 row: 0 column: 07
High quality sequence stop: 718.
Location/Qualifiers
1..780
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/mol_type="mRNA"
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/clone="IMAGE:4612062"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
$fil (ggcgccctggcc); Site 2: $fil (ggcgccatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATATATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65

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FEATURES

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source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4612062"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
$fil (ggcgccctggcc); Site 2: $fil (ggcgccatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCGCATATATGCGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65

```

ORIGIN

kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

Query Match 93.7%; Score 598; DB 12; Length 780;
 Best Local Similarity 99.8%; Pred. No. 2e-155;
 Matches 609; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy      30 TCCATTCATGCTGGAATCTGTCGAACCCAGGTGAGAAATGCTTTAAAGTAGACTAG 89
Db      1 TCCATTCATGCTGGAATCTGTCGAACCCAGGTGAGAAATGCTTTAAAGTAGACTAG 60
Qy      90 TATCAGAACGCTCTGGAGATTAAGCATATGCTGGATACCAATGAATACCTCT 149
Db      61 TATCAGAACGCTCTGGAGATTAAGCATATGCTGGATACCAATGAATACCTCT 120
Qy      150 CAAGGATGTAAGCTTTCTCATGAGAAATGTTCCCAACAGAAACAAAGATTC 209
Db      121 CAAGGATGTAAGCTTTCTCATGAGAAATGTTCCCAACAGAAACAAAGATTC 180
Qy      210 CCAATGCTTACTTTCGAATGTAACCGAGGGTATCATCTGTTGGTTGCTACAGACC 269
Db      181 CCAATGCTTACTTTCGAATGTAACCGAGGGTATCATCTGTTGGTTGCTACAGACC 240
Qy      270 TTCAAAATATCACAACCTTCTCTGCTGTTGAGTGAATCAGCCATAGAAATGA 329
Db      241 TTCAAAATATCACAACCTTCTCTGCTGTTGAGTGAATCAGCCATAGAAATGA 300
Qy      330 CCGGATCAACATGCTTCTTCTTAATGACCAACCTGGAATTTTAAATCCCTTC 389
Db      301 CCGGATCAACATGCTTCTTCTTAAATGACCAACCTGGAATTTTAAATCCCTTC 360
Qy      390 CACACTTGAACCAACCCATGAGACCCATCTGAGCCATCTGATATATATTTGGTAT 449
Db      361 CACACTTGAACCAACCCATGAGACCCATCTGAGCCATCTGATATATATTTGGTAT 420
Qy      450 ATTTGCAATCATATGTTGCAATTCACATGATATTTTATCAGGATCTGCAACCTAG 509
Db      421 ATTTGCAATCATATGTTGCAATTCACATGATATTTTATCAGGATCTGCAACCTAG 480
Qy      510 AAGAAAGAACAAAGAACATCTGAAGTGAATGCTGAAGATGTAAGTGAATGAT 569
Db      481 AAGAAAGAACAAAGAACATCTGAAGTGAATGCTGAAGATGTAAGTGAATGAT 540
Qy      570 CACATTTGAATTAAGGCAATCCCTCTGATATCCCTGAGACATGAAGGG-CCGCAATATATGA 628
Db      541 CACATTTGAATTAAGGCAATCCCTCTGATATCCCTGAGACATGAAGGGCAATATATGA 600
Qy      629 TGCCTTCATG 638
Db      601 TGCCTTCATG 610

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RESULT 10
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DEFINITION
602464526P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592575 5',
mRNA sequence.
ACCESSION
BG400319
VERSION
BG400319.1 GI:13293767
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 791)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov

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Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1331 row: c column: 08
High quality sequence stop: 711.

FEATURES

Source

Location/Qualifiers

1..791

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4592575"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcggcc); Site 2: SfiI (ggccatctggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."

ORIGIN

Query Match 92.9%; Score 593; DB 12; Length 791;
Best Local Similarity 99.4%; Pred. No. 4.9e-154;
Matches 637; Conservative 0; Mismatches 0; Indels 4; Gaps 4;

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QY 1 ATGTTGGCTGCTCTTTTCTGTCGTCATTCATGCTGAAGCTCTGCAACAGGT 60
DB 31 ATGTTGGCTGCTCTTTTCTGTCGTCATTCATGCTGAAGCTCTGCAACAGGT 90
QY 61 GCAGAAATGCTTTAAAGTGAAGTCTAGTATGAGCAAGCTCTGGAGATTAAGCAT 120
DB 91 GCAGAAATGCTTTAAAGTGAAGTCTAGTATGAGCAAGCTCTGGAGATTAAGCAT 150
QY 121 GCCTGGATACCAATGAAGTACCTCTTCAAGGATGAGCTTTCTCCATGAGAAA 180
DB 151 GCCTGGATACCAATGAAGTACCTCTTCAAGGATGAGCTTTCTCCATGAGAAA 210
QY 181 GTTCCCAACAGAGAGCAAGCAATTTCCATGCTCTTGAATGAATACCAAGAG 240
DB 211 GTTCCCAACAGAGAGCAAGCAATTTCCATGCTCTTGAATGAATACCAAGAG 270
QY 241 GTATCATTTGGTTGGTTTACAGACCTTCAAAAATATCAACCTTCCTGCTGAG 300
DB 271 GTATCATTTGGTTGGTTTACAGACCTTCAAAAATATCAACCTTCCTGCTGAG 330
QY 301 GTGCAATCAGCCATAGATGAGCAAGAACCGATCAACATGCTTTCTTAATGAC 360
DB 331 GTGCAATCAGCCATAGATGAGCAAGAACCGATCAACATGCTTTCTTAATGAC 390
QY 361 CAAACTCTGAATTTTAAAAATCCCTTCACTTGAACCAACCATCTGAG 420
DB 391 CAAACTCTGAATTTTAAAAATCCCTTCACTTGAACCAACCATCTGAG 450
QY 421 CCCATCTGATTTATATATT-6GTGATATTTTTCATCATATGTTGCAATGCACT 479
DB 451 CCCATCTGATTTATATATTGCGTGATATTTTTCATCATATGTTGCAATGCACT 510
QY 480 ACTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAAAGAAACCATCTGAGTGA 539
DB 511 ACTGA-TTTATCAGGATCTGGCAACGTAGAGAAAGAAAGAAACCATCTGAGTGA 569
QY 540 TGAAGCTGAAGATAGTGTGAAGAAATGATCAATTTGAAATGGCAATCCCTGAGTCC 599
DB 570 TGAAGCTGAAGATAGTGTGAAGAAATGATCAATTTGAAATGGCAATCCCTGAGTCC 629
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QY 600 CTTGACATGTAAGGG-GGGCATATTAA-TGATGCTTCATG 638
DB 630 CTTGACATGTAAGGGGAGGAGATATTAAAGTATGCTTCATG 670

RESULT 11

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 850)

NIH-MGC http://imgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC).

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@b-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: L10M1364 row: n column: 14

High quality sequence stop: 681.

Location/Qualifiers

1..850

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4613965"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NIH_MGC_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccgctcggcc); Site 2: SfiI (ggccatctggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCCAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."

ORIGIN

Query Match 92.7%; Score 591.6; DB 12; Length 850;
Best Local Similarity 97.5%; Pred. No. 1.2e-153;
Matches 622; Conservative 0; Mismatches 14; Indels 2; Gaps 2;

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QY 1 ATGTTGGCTGCTCTTTTCTGTCGTCATTCATGCTGAAGCTCTGCAACAGGT 60
DB 31 ATGTTGGCTGCTCTTTTCTGTCGTCATTCATGCTGAAGCTCTGCAACAGGT 95
QY 36 ATGTTGGCTGCTCTTTTCTGTCGTCATTCATGCTGAAGCTCTGCAACAGGT 120
DB 61 GCAGAAATGCTTTAAAGTGAAGTCTAGTATGAGCAAGCTCTGGAGATTAAGCAT 155
QY 96 GCAGAAATGCTTTAAAGTGAAGTCTAGTATGAGCAAGCTCTGGAGATTAAGCAT 180
DB 121 GCCTGGATACCAATGAAGTACCTCTTCAAGGATGAGCTTTCTCCATGAGAAA 215
QY 156 GCCTGGATACCAATGAAGTACCTCTTCAAGGATGAGCTTTCTCCATGAGAAA 240
DB 181 GTTCCCAACAGAGAGCAAGCAATTTCCATGCTCTTGAATGAATACCAAGAG 275
QY 216 GTTCCCAACAGAGAGCAAGCAATTTCCATGCTCTTGAATGAATACCAAGAG 300
DB 241 GTATCATTTGGTTGGTTTACAGACCTTCAAAAATATCAACCTTCCTGCTGAG 330
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Db 276 GATATTCGTTGGTTGTTACAGACCCCTTCAAAAATCAACCCCTTGGCTGAG 335
Qy 301 GTGCAATTCAGCCATTAAGATGAACAGAACCCGATCAACATGCTTCTTAAATGAC 360
Db 336 GTGCAATTCAGCCATTAAGATGAACAGAACCCGATCAACATGCTTCTTAAATGAC 395
Qy 361 CAAACCTGGAAATTTTAAATCCCTTCACACCTTGACACCCATGAGCCATCTGTG 420
Db 396 CAAACCTGGAAATTTTAAATCCCTTCACACCTTGACACCCATGAGCCATCTGTG 455
Qy 421 CCAATCTGATTTATTAATTTGTTGATTTTTCATCATCATGATTCATTCATCACTA 480
Db 456 CCAATCTGATTTATTAATTTGTTGATTTTTCATCATCATGATTCATTCATCACTA 515
Qy 481 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAAGAAAGCAATCTGAATGAT 540
Db 516 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAAGAAAGCAATCTGAATGAT 575
Qy 541 GAGCCTGAAGATAGTGTGAAGACATGATCAATGAAATGATCCCTCTGATGCC 600
Db 576 GAGCCTGAAGAT-AGTGTGAAGACATGATCAATGAAATGAT-CCCTCTGATGCC 633
Qy 601 CTGACATGAAGGGGCGCATATTAATGATGCTTCATG 638
Db 634 TGGACATGAAGGAGGCGCATATTAATGATGCTTCATG 671

RESULT 12
Bg399473 808 bp mRNA linear EST 12-MAR-2001
LOCUS Bg399473
DEFINITION 602441126F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557073 5',
mRNA sequence.
ACCESSION Bg399473
VERSION Bg399473
KEYWORDS GI:13293021
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 808)
NIH-MGC http://imgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM1260 row: 1 column: 02
High quality sequence stop: 637.
Location/Qualifiers
1. 808

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4557073"
/lab_host="DH10B (T1 phage-resistant)"
/note="NIH_MGC_75"
/clone_lib="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccgcgcgc); Site 2: SfiI (ggcgccatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAAGCGCATTAATGATG-3' and 3' adaptor sequence:
5'-ATCTGAGGCGCGAGCGCGCATTAATGATG-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 91.8%; Score 586; DB 12; Length 808;
Best Local Similarity 96.5%; Pred. No. 4,4e-152;
Matches 610; Conservative 0; Mismatches 20; Indels 2; Gaps 1;

Qy 1 ATGTGTGGCTGCTCTTTTCTGTGAGTGCATTCATGCTGAATCTGTCAACAGT 60
Db 32 ATGTGTGGCTGCTCTTTTCTGTGAGTGCATTCATGCTGAATCTGTCAACAGT 91
Qy 61 GCGAAATAGCTTTTAAAGTGAAGCTTAATGCAACAGCTCTGGAGATTAAGCAT 120
Db 92 GCGAAATAGCTTTTAAAGTGAAGCTTAATGCAACAGCTCTGGAGATTAAGCAT 151
Qy 121 GCGTGGATTCAGATGAAGATTCCTTCAAGCGATGGAGCTTCTCCATGAGAAA 180
Db 152 GCGTGGATTCAGATGAAGATTCCTTCAAGCGATGGAGCTTCTCCATGAGAAA 211
Qy 181 GTTCCCAACAGAGAGAGAGAAATTTCCATCTCTTCAATGTAACCAAGAG 240
Db 212 GTTCCCAACAGAGAGAGAGAAATTTCCATCTCTTCAATGTAACCAAGAG 271
Qy 241 GTATCATTTCTGTTTGTGTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 300
Db 272 GTATCATTTCTGTTTGTGTACAGACCTTCAAAAATCAACCTTCTGCTGTGAG 331
Qy 301 GTGCAATTCAGCCATTAAGATGAACAGAACCCGATCAACATGCTTCTTAAATGAC 360
Db 332 GTGCAATTCAGCCATTAAGATGAACAGAACCCGATCAACATGCTTCTTAAATGAC 391
Qy 361 CAAACCTGGAAATTTTAAATCCCTTCACACCTTGACACCCATGAGCCATCTGTG 420
Db 392 CAAACCTGGAAATTTTAAATCCCTTCACACCTTGACACCCATGAGCCATCTGTG 451
Qy 421 CCAATCTGATTTATTAATTTGTTGATTTTTCATCATCATGATTCATTCATCACTA 480
Db 452 CCAATCTGATTTATTAATTTGTTGATTTTTCATCATCATGATTCATTCATCACTA 511
Qy 481 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAAGCAATCTGAATGAT 540
Db 512 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAAAGCAATCTGAATGAT 571
Qy 541 GAGCCTGAAGATAGT-GTGAAGACATGATCAATTAATGATGATCCCTCTGATG 598
Db 572 GAGCCTGAAGATAGTGTGAAGACATGATCCATCTGAATGATGATGATGATG 631
Qy 599 CCTGACATGAAGGGGCGCATATTAATGATG 630
Db 632 CCTGACATGAAGGAGGCGCATATTAATG 663

RESULT 13
Bg399402 736 bp mRNA linear EST 12-MAR-2001
LOCUS Bg399402
DEFINITION 602441161F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557015 5',
mRNA sequence.
ACCESSION Bg399402
VERSION Bg399402
KEYWORDS GI:13292850
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 736)
NIH-MGC http://imgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strauberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Sequencing by: Incyte Genomics, Inc.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLMT at: <http://image.llnl.gov>
 Plate: L1CM1260 row: 1 column: 16
 High quality sequence, stop: 661.

FRATRES
SOURCE

Sources

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/organism="Homo sapiens"
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/clone="IMAGE:4557015"
/lab_host="MDH10B (T1 phage-resistant)"
/clone_lib="NH_MGC_75"
/name="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggcgcacgcgcgc); Site_2: SfiI (ggcgcacgcgc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGCGCCATTATGAGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCGCAGGCGGCCGACATG-dt(30)BA-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-5.4 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NH_MGC Library."

```

ORIGIN

Query Match	91.8%	Score 585.8;	DB 12;	Length 736;
Best Local Similarity	99.2%;	Pred. No. 4.9e-15;		
Matches 620; Conservative	0;	Mismatches 2;	Indels 3;	Gaps 3.

Qy	12	GCCTCTTTTTCGCGA	CTGCATTCATGCTGAA	CTCTGTCAACAGAGTCAGAAAATGC	71
Db	3	GCCTCTTTTTCGCGA	CTGCATTCATGCTGAA	CTCTGTCAACAGAGTCAGAAAATGC	62
Qy	72	TTTTAAAGTGA	CTTAGTATCAGAACAGCTCTGAGATAAAGCATATGCTTGGATAC	131	
Db	63	TTTTAAAGTGA	CTTAGTATCAGAACAGCTCTGAGATAAAGCATATGCTTGGATAC	122	
Qy	132	CAATGAAAGATATACCTCTTCAAAAGCATGATGCTTCCCATGAGAAAAGTTCCCAACAG	191		
Db	123	CAATGAAAGATATACCTCTTCAAAAGCATGATGCTTCCCATGAGAAAAGTTCCCAACAG	182		
Qy	192	AGAGCAACAGAAATTTCCATGCTCTACTTTCAGATGTAACCCAGAGGATCATTCG	251		
Db	183	AGAGCAACAGAAATTTCCATGCTCTACTTTCAGATGTAACCCAGAGGATCATTCG	242		
Qy	252	GTTTGATGTTACAGACCCCTTCAAAAATCACAACCCCTCTGCTGTGAGTGCAATCAGC	311		
Db	243	GTTTGATGTTACAGACCCCTTCAAAAATCACAACCCCTCTGCTGTGAGTGCAATCAGC	302		
Qy	312	CATTAAGATGAAACAGAAACCGGATCAACAATGCTTCTTCAATATGACCAAACTCTGGA	371		
Db	303	CATTAAGATGAAACAGAAACCGGATCAACAATGCTTCTTCTTCAATATGACCAAACTCTGGA	362		
Qy	372	ATTTTAAAAATCCCTTCACA	CTTGACAACAACCCATGACCCCATCTGAT	431	
Db	363	ATTTTAAAAATCCCTTCACA	CTTGACAACAACCCATGACCCCATCTGAT	422	
Qy	432	TATTAATATTTGGTGTGATATTTTGCATCATATATTTGCAATTTGCACTACATATTTATC	491		
Db	423	TATTAATATTTGGTGTGATATTTTGCATCATATATTTGCAATTTGCACTACATATTTATC	482		
Qy	492	AGGATCTGGCAACGTAGAG-AAAGAACAAAGAACATCTGAAGTGAACGCTGAG	550		
Db	483	AGGATCTGGCAACGTAGAG-AAAGAACAAAGAACATCTGAAGTGAACGCTGAG	542		
Qy	551	ATAAGTGTGAAAACATGATCACA-TTGAAAATGGCATCCCTCTGATCCCTTGACATG	609		
Db	543	ATAAGTGTGAAAACATGATCACA-TTGAAAATGGCATCCCTCTGAT-CCCTGACATG	601		
Qy	610	AAAGGGGCAATTTAATGATGCTT	634		
Db	602	AAAGGGGCAATTTAATGATGCTT	626		

RESULT 14	
BG427839	
LOCUS	BG427839
DEFINITION	60250152PFI NIH MGC 75 Homo sapiens CDNA clone IMAGE:4615156 5', mRNA sequence.

VERSION	BC427839.1	GI:13334345
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE	1 (bases 1 to 859)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES

Source

Source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4615156"
/lab_host="MDH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/notes="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgatcattggcc); Site_2: SfiI (ggcgatcattggcc); 5' adaptor sequence used in cloning as follows: 5' adaptor sequence: 5'-CAGGCGCATTAAGGCC-3' and 3' adaptor sequence: 5'-ATTCTGAGAGCCCGCAGGCGCGCGCAGCATG-dt(30)BH-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.6 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH MGC Library."

```

ORIGIN

Query Match	91.7%	Score 584.8;	DB 12;	Length 859;
Best Local Similarity	-99.2%;	Pred. No. 9.5e-152;		
Matches 619; Conservative	0;	Mismatches 2;	Indels 3;	Gaps 3;

QY	14	TCCTTTTCTGATGCTGCAATCATGCTGAACCTGTCAACCAAGGTCACAGAAAATGCTT	73
Db	2	TCCTTTTCTGTGATGCTGCATTAATGCTGAACCTGTCAACCAAGGTCACAGAAAATGCTT	61
QY	74	TTAAAGTAGACTAGTATCAGAACAGCTCTGGAGATTAAGCATATGCTGGATATACA	133
Db	62	TTAAAGTAGACTAGTATCAGAACAGCTCTGGAGATTAAGCATATGCTGGATATACA	121
QY	134	ATGAAGATATCTCTCAAAAGCGATGGAGCTTCTCCATGAGAAAAGTTCACAAGAG	193
Db	122	ATGAAGATATCTCTCAAAAGCGATGGAGCTTCTCCATGAGAAAAGTTCACAAGAG	181
QY	194	AAGCAACGAAATTTCCATGCTCTAAGCTTGGCATGTAAACCGAAGGGTATCAATTCGT	253
Db	182	AAGCAACGAAATTTCCATGCTCTAAGCTTGGCATGTAAACCGAAGGGTATCAATTCGT	241
QY	254	TTGGGTATACAGACCCCTCAAAAAATCAACCCCTCTGCTGTGTGAGGTGCATACAGCA	313
Db	242	TTGGGTATACAGACCCCTCAAAAAATCAACCCCTCTGCTGTGTGAGGTGCATACAGCA	301
QY	314	TGAGATGACAGAAACCGAGTCAACATGCTTCTTCTAATACCAAACTCTGAGAT	373

REFERENCE
1 (bases 1 to 888)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE
JOURNAL
COMMENT
Eukaryote; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLI at:
http://image.llnl.gov
Plate: ILNLI331 row: p column: 11
High quality sequence stop: 723.
Location/Qualifiers

FEATURES
SOURCE

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/clone="IMAGR:4592890"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_75"
/note="Organ: Kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgccctggcc); Site 2: SfiI (ggcgctatggc); 5' and
3' adaptor were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTTATGCCC-3' and 3' adaptor sequence:
5'-ATCTAGAGCGCGAGCGCGGACATG-DT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
```

ORIGIN

Query Match 90.3%; Score 576; DB 12; Length 888;
Best Local Similarity 97.7%; Pred. No. 2,7e-149;
Matches 627; Conservative 0; Mismatches 10; Indels 5; Gaps 4;

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1 ATGTTGAGCTCTCTTTTCTGTTGACCTGCAATTCATGAACTCTGCAACAGT 60
36 ATGTTGAGCTCTCTTTTCTGTTGACCTGCAATTCATGAACTCTGCAACAGT 95
61 GCAGAAATGCTTTTAAAGTGAAGTGA-CTATCGAAGACGCTCGGAGATTAAGCATA 119
96 GCAGAAATGCTTTTAAAGTGAAGTGA-CTATCGAAGACGCTCGGAGATTAAGCATA 155
120 TGCCGGAATACCAATGAAGATACCTCTTCAAGACGATGTTCTCCATGAGAA 179
156 TGCCGGAATACCAATGAAGATACCTCTTCAAGACGATGTTCTCCATGAGAA 215
180 AGTTCCCAAGAGAGCAAGCAAGAAATTTCCATGCTCTTCAATGTAACCAAG 239
216 AGTTCCCAAGAGAGCAAGCAAGAAATTTCCATGCTCTTCAATGTAACCAAG 275
240 GGTATCATCTGTTTGGTTAGTACAGCTTCAAAAATCAACCTTCCGCTGTTGA 299
276 GGTATCATCTGTTTGGTTAGTACAGCTTCAAAAATCAACCTTCCGCTGTTGA 335
300 GGTGCAATCAGCAATGAAGATGAACAGACCGATCAACATGCTTCTTAAATGA 359
336 GGTGCAATCAGCAATGAAGATGAACAGACCGATCAACATGCTTCTTAAATGA 395
360 CCAAACTCTGAAATTTTAAATCCCTTCAACATGCAACCAATGCAACCAATGCT 419
396 CCAAACTCTGAAATTTTAAATCCCTTCAACATGCAACCAATGCAACCAATGCT 455
420 GCCCATCTGATATATATTTGGTGTATATTTGATCATCATAGTTGCAATGGAGT 479
456 GCCCATCTGATATATATTTGGTGTATATTTGATCATCATAGTTGCAATGGAGT 515
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480 ACTGATTTTATCAGGATCTGGCAACGTAAAGAAAGAAACCAACCATGTAAGTGA 539
516 ACTGATTTTATCAGGATCTGGCAACGTAAAGAAAGAAACCAACCATGTAAGTGA 575
540 TGAGCTG-AGATTAAGTGAAGAAACATGATCAATGAAATGTCCTCTGATC 598
576 TGAGCTGCAAGATTAAGTGAAGAAACATGATCAATGAAATGTCCTCTGATC 634
599 CCTGGAATGAAGG--GGGCAATATTAATGATGCTTCAATG 638
635 CCTGGAATGAAGGAGGCAATATTAATGATGCTTCAATG 676

RESULT 20
BM811234 1081 bp mRNA linear EST 05-MAR-2002
LOCUS AGNCOURT 6489717 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5723829
DEFINITION 5' mRNA sequence.
ACCESSION BM811234 GI:19128057
VERSION BM811234
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
1 (bases 1 to 1081)
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
TITLE
JOURNAL
COMMENT
Eukaryote; Metazoa; Chordata; Cranial; Vertebrata; Euteleostomi;
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNLI at:
http://image.llnl.gov
Plate: ILNLI212 row: b column: 22
High quality sequence stop: 721.
Location/Qualifiers

FEATURES
SOURCE

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1. 1081
/organism="Homo sapiens"
/mol_type="rRNA"
/db_xref="taxon:9606"
/clone="IMAGR:5723829"
/lab_host="DH10B"
/clone_id="NIH_MGC_125"
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(Bcovr site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalised and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."
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ORIGIN

Query Match 89.6%; Score 571.4; DB 12; Length 1081;
Best Local Similarity 99.7%; Pred. No. 5.3e-146;
Matches 583; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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55 CAGGTGCAAGAAATGCTTTTAAAGTGAAGTATGATCAAGACGCTTGGAGATTA 114  
165 CAGGTGCAAGAAATGCTTTTAAAGTGAAGTATGATCAAGACGCTTGGAGATTA 224  
115 GGTATGCTGGAATACCAATGAAGATACCTCTTCAAGCGATGATCTTCTCATG 174  
225 GGTATGCTGGAATACCAATGAAGATACCTCTTCAAGCGATGATGCTTCTCATG 284  
175 AGAAAGTTCCCAAGAGAGCAAGAAATTTCCATGCTTCTTGAATGTAAC 234
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Db	Accession	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	285	AGAAAAGTCCCAACAGAGAAGCAACAGAAATTTTCCCATGCTACTTGTGAATGTAAAC	344					
Qy	235	CAGAGGGTATCATCTCTGGTTTGCTGTACAGACCCCTTCAAAAATTCACACCCCTTCGTCT	294					
Db	345	CAGAGGGTATCATCTCTGGTTTGCTGTACAGACCCCTTCAAAAATTCACACCCCTTCGTCT	404					
Qy	295	GTTGAGGTGCATCAGCCATTAAGAAATGAACAAGAACCGATCAACAATGCTCTTCTTA	354					
Db	405	GTTGAGGTGCATCAGCCATTAAGAAATGAACAAGAACCGATCAACAATGCTCTTCTTA	464					
Qy	355	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACATTGCAACCAACCATGACCCA	414					
Db	465	AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACATTGCAACCAACCATGACCCA	524					
Qy	415	TCCTGTGCCAATCTGATATTAATATTTGGTGTGATATTTTGCATCATCATGTGTCATAT	474					
Db	525	TCCTGTGCCAATCTGATATTAATATTTGGTGTGATATTTTGCATCATCATGTGTCATAT	584					
Qy	475	GCACTACTGATTTTATCAGGATCTGCGACGTAGAGAGAGAAACAAGAACCATCTGAA	534					
Db	585	GCACTACTGATTTTATCAGGATCTGCGACGTAGAGAGAGAAACAAGAACCATCTGAA	644					
Qy	535	GTGATATACGCTGAGATTAAGTGTGAAAACATGATCACATTTGAATAATGCAATCCCTCT	594					
Db	645	GTGATATACGCTGAGATTAAGTGTGAAAACATGATCACATTTGAATAATGCAATCCCTCT	704					
Qy	595	GATCCCTCTGACATGAAGGCGGATTAATGATGCTTCATG	638					
Db	705	GATCCCTCTGACATGAAGGCGGATTAATGATGCTTCATG	749					
RESULT 21								
LOCUS	BG429011	678 bp	mRNA	linear	EST 14-MAR-2001			
DEFINITION	602501924P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4615540 5',							
ACCESSION	BG429011							
VERSION	BG429011.1	GI:13335517						
KEYWORDS	BST.							
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.							
TITLE	1 (bases 1 to 678)							
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/ .							
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)							
	Unpublished (1999)							
	Contact: Robert Strausberg, Ph.D.							
	Email: cs9ab@remail.nih.gov							
	Tissue Procurement: CLONTECH Laboratories, Inc.							
	cDNA Library Preparation: CLONTECH Laboratories, Inc.							
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)							
	DNA Sequencing by: Incyte Genomics, Inc.							
	Clone distribution: MGC clone distribution information can be							
	found through the I.M.A.G.E. Consortium/LNLN at:							
	http://image.llnl.gov							
	Plate: ILGM1368 row: p column: 05							
	High quality sequence stop: 672.							
FEATURES								
source	1..678							
	Location/Qualifiers							

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Location/Qualifiers
1..678
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4615540"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NH MGC 75"
/note="Organ: kidney; Vector: pDMR-LIB (Clontech); Site_1:1; Site_2:5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATTAAGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGAGGCGCGCGGACATG-dt(30)BA-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.66 kb, or range 0.5-4.0 kb). 15/15 colonies contained inserts

```

ORIGIN

by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto CA). Note: this is a NIH_MGC Library."

Query Match	88.14;	Score 562;	DB 12;	Length 678;

Matches 615; Conservative 0; Mismatches 17; Indels 4; Gaps 4.

5 TGTGGCTGCTCTTTTCTGTGACTGCCATTCATGCTGAAGTCTGTCAACCAAGTGCAG 64

34 TGTGGCTGCTCTTTTCTCGGTGACCGCATTCATGCTGAATCTGTCAACGAGTGCAG 93

65 AAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGAGATAAGCATAATGCCCT 12

Db 94 AAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCCCT 15

125 GGGATACCAATGAGAATACCTCTTCAAAGCGATGTAGCTTTCTCCATGAGAAAGTTC 18

Db 154 GGGATACCAATGAAGATACTTTCAAAGCGATGGTAGCTTCTCCATGAGAAAGTTC 21

185 CCAACAGAGAGCAACAGAAATTTCCTACTTTGCAATGTAAACCAGAGGCTAT 24

Db 214 CCACAGAGAGCAACAGAATTTCCTACTTTGCAATGTAAACCAGAGGGTAT 27

245 CATTCTGGTTTGTGGTTACAGACCCCTTCAAAAATCACACCCCTTCCCTGCTGTTGAGGTC 30

Db 274 CATTCTGTTGTTACAGACCCCTTCAAAAAATCAGACCCCTTCCTGCTGTGAGGTC 33

305 AATCAGCCATAGAATGAACAAGAACCGGATCAACAATGCCCTCTTTCTAATGACCAAA 36

Db 334 AATCAGCCATAAGATGAACAAGAACCGGATCAACAATGCCCTTCTTCTAAATGACCAA 339

365 CTCTGGATTTTTAAATCCCTTCCACACTTGCACCCACCCATGGAACCATCTGACCCTCA 42

Db 394 CTTGGATTTTTAAATCCCTTCCACACTTGCACCCACCATTGGACCCATCTGTCTCA 45

425 TCTGGATTATATTTGGTGTGATATTTGCATCATCATAGTTGCAATTCACCTACCA 488

Db 454 TCTGGATTATATTTCGTGATATTTGCATCATCATAGTTGCAATTGCACACIAGA 51

485 TTTTATCAGGATC-TGGCAACGTAGAAGAAGACCAAGAACCATTCTGAAGTGGATGAC 54

Db 514 TTTTATCAGCGATCTGGCAACGTAGAGAAGAAGACAAAGAA-CATCTGAGTGGATGA-5'

544 GCTGAAGTAACTGTGAACATGATCACAATTGAATGGCAATCCCTCTGATCCCTG

Db 572 GCTGAGATTAAGTGTGAACACATGATCAACATGAAATGATCCCTCTGATCCCGTG 63

604 GACATGAAGGC-GGGCATATTATGATGCCCTTCATG 638

Db 632 GACATGAAGGAGGCATATTAAAGATGCTTCAATG 667

РЕСПУБЛИКА

BG432624
 1 OCT 68
 BC432624
 602 hr
 MPNB
 11 near
 EST 14-MAR-70

DEFINITION 602500789P1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4614070 5',
MBNT 8027899

ACCESSION	BG432624
VERSION	BG432624 1
CT	CT:13339130

KEYWORDS EST.
SOURCE HOMO sapiens (human)

ORGANISM Homo sapiens
Bukarvota: Metazoa: Chordata: Vertebrata: Buteleostomi:

PREFERENCE 1 (pages 1 to 602)
Mammalia; Rutherford; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS NIH-MGC <http://mgc.hci.nih.gov/>;
TITL National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
unpublished (1999)

COMMENT
Contact: Robert Strausberg, Ph.D.

Email: cgapds-1@mail.nih.gov
Tissue Procurement: CLONTech Laboratories, Inc.

Dh 381 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTCTTCTTAATATGAC 440
Qy 361 CAACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 420
Dh 441 CAACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 500
Qy 421 CCACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 480
Dh 501 CCACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 559
Qy 481 CTGATTTTATCAGGATCTGGCAACCTAGAA---GAAAGACAAAGAACCATCTGAGTG 537
Dh 560 CTGA-TTATACGAGGATCTGGCAACCTAGAAAGGAAACCAATCTGAGTG 618
Qy 538 GATGACCTGAAGAT-AGTGTGAAGAACTGATCAATTTGA-AAATGCAATCCCTGAG 595
Dh 619 GATGACCTGAAGATCACTGTGAAGAACTGATCAATTTGA-AAATGCAATCCCTGAG 678
Qy 596 ATCCCTGGAACATGAA--GGGGGCAATTTATGATGCTCTGAGT 638
Dh 679 ATGCTCTGACATTAAGAGAGGATCTTAATGATGCTCTGAGT 723

RESULT 24
BG399975 884 bp mRNA linear EST 12-MAR-2001
LOCUS 60244202881 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4557751 5',
DEFINITION mRNA sequence.

ACCESSION BG399975
VERSION BG399975.1 GI:13293423
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 884)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Clontech Laboratories, Inc.
cDNA Library Preparation: Clontech Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inqye Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1262 row: h column: 08
High quality sequence stop: 590.
Location/Qualifiers

FEATURES
SOURCE 1..884

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/db_xref="taxon:9606"
/clone="IMAGE:4557751"
/lab_host="DH10B (T1 phage-resistant)"
/clone_id="NIH_MGC_75"
/note="Organ: kidney; Vector: pDMR-LIB (Clontech); Site 1:
SfiI (ggcgccgcgcgc); Site 2: SfiI (ggcgccgcgcgc); 5' and
3' adaptor were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCCTTATGAGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGCCGACATG-3' (where B = A,
C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 85.6%; Score 546.2; DB 12; Length 884;
Best Local Similarity 94.6%; Pred. No. 5.4e-141;
Matches 599; Conservative 0; Mismatches 28; Indels 6; Gaps 3;

Qy 1 AAGTGTGCTGCTCTTTTCTGAGTCCATTCATGCTGACCTGTCACCAAGT 60
Dh 32 AAGTGTGCTGCTCTTTTCTGAGTCCATTCATGCTGACCTGTCACCAAGT 91
Qy 61 GCAAGAAATGCTTTAAAGTGAAGCTTATGATGAGCAAGCTTGGAGATTAAGCTAT 120
Dh 92 GCAAGAAATGCTTTAAAGTGAAGCTTATGATGAGCAAGCTTGGAGATTAAGCTAT 151
Qy 121 GCTGTGATACCAATGAATACCTCTCAAGAGAGTGTAGCTTCTTCATGAGAAA 180
Dh 152 GCTGTGATACCAATGAATACCTCTCAAGAGAGTGTAGCTTCTTCATGAGAAA 211
Qy 181 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTTCTTCAATGTAACCAAGAG 240
Dh 212 GTTCCCAAGAGAGCAAGAAATTTCCATGCTCTTCTTCAATGTAACCAAGAG 271
Qy 241 GTATCATCTGTTGTGTGTTAAGACCTTCACAAATATCAACCTTCTGCTGTAG 300
Dh 272 GTATCATCTGTTGTGTGTTAAGACCTTCACAAATATCAACCTTCTGCTGTAG 331
Qy 301 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTCTTCTTAATGAC 360
Dh 332 GTGCAATCAGCCATTAAGATGAACAAGAACCGATCAACATGCTCTTCTTAATGAC 391
Qy 361 CAACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 420
Dh 392 CAACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 451
Qy 421 CCACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 480
Dh 452 CCACTCTGGAATTTTAAATCCCTTCACATTCGACCAATGAGCCATCTGAG 510
Qy 481 CTGATTTTATCAGGATCTGGCAACCTAGAAAGGAAACCAATCTGAGTGAGT 540
Dh 511 CTGATTTTATCAGGATCTGGCAACCTAGAAAGGAAACCAATCTGAGTGAGT 570
Qy 541 GACGCTGAAGATTAAGTGAAGAAATGATGATCAATGAAATGAGCATCTGATCCC 600
Dh 571 GACGCTGAAGATTAAGTGAAGAAATGATGATCAATGAAATGAGCATCTGATCCC 625
Qy 601 CTGACATGAAGAGGAGCATTTATTAATGATGCTT 633
Dh 626 CTGACATGAAGAGGAGCATTTATTAATGATGCTT 658

RESULT 25
AV653898 735 bp mRNA linear EST 15-JAN-2002
LOCUS AV653898 GUC Homo sapiens cDNA clone GUCD908 3', mRNA sequence.
DEFINITION AV653898
ACCESSION AV653898
VERSION AV653898.1 GI:9874912
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 735)
Xiao, H., Qu, J., Liu, P., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,
Shen, K., Lu, G., Pu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,
Hu, G., Gu, J., Chen, Z., and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level
by comparing gene expression profiles of hepatocellular carcinoma
with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
JOURNAL MEDLINE PUMED
11752456
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)

FEATURES

- Fax: 86-21-50801922
- Email: hangy@chgc.sh.cn
- This clone is available at CHGC in Shanghai.
- Location/Qualifiers

ORIGIN

```

Query Match      84.8%   Score 541;  DB 9;   Length 735;
Best Local Similarity 99.1%   Pred. No. 1.5e-139;
Matches 574;  Conservative 0;  Mismatches 2;  Indels 3;  Gaps 3;

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Qy	1	ATGTTGAGCGCTCTTTTCTGGTACTGCATTATGCGAATCTGTCCACAGGT	60
Db	61	ATGTTGAGCGCTCTTTTCTGGTACTGCATTATGCGAATCTGTCCACAGGT	120
Qy	61	GCAGAAAATGCTTTTAAAGTAGAGACTTAGATCAGAACGCTCTGGAGATTAACATAT	120
Db	121	GCAGAAAATGCTTTTAAAGTAGAGACTTAGATCAGAACGCTCTGGAGATTAACATAT	180
Qy	121	GCTTGGATACCAATGAAATACCTTTCAAAGGATGTAGCTTTTCTCCATGAGAAA	180
Db	181	GCTTGGATACCAATGAAATACCTTTCAAAGGATGTAGCTTTTCTCCATGAGAAA	240
Qy	181	GTTCCCAACAGAGAAGCAAGAAATTTCCATGTCTACTTTCGAAATGTAACACAGAG	240
Db	241	GTTCCCAACAGAGAAGCAAGAAATTTCCATGTCTACTTTCGAAATGTAACACAGAG	300
Qy	241	GTATCATTTCTGTTGTGTGATTACAGACCTTTCAAAAATTCACACCTTCTGTGTAG	300
Db	301	GTATCATTTCTGTTGTGTGATTACAGACCTTTCAAAAATTCACACCTTCTGTGTAG	360
Qy	301	GTGCAATCAGCCTTAAGATGAAAGAAACCGGATCAACATGCTTCTTAAATAC	360
Db	361	GTGCAATCAGCCTTAAGATGAAAGAAACCGGATCAACATGCTTCTTAAATAC	420
Qy	361	CAAACTCTGGAATTTTAAAAATCCCTTCCACTGTGACCAACCCATGCACTGTG	420
Db	421	CAAACTCTGGAATTTTAAAAATCCCTTCCACTGTGACCAACCCATGCACTGTG	480
Qy	421	CCCATCTGATTAATTAAT-TTGGTGTGATATTGTGCATCATATAGTGCATGCACT	479
Db	481	CCCATCTGATTAATTAATNNGTGTGATTTTGTGCATCATATAGTGCATGCACT	540
Qy	480	ACTGATTTTATCA-GGGATCTGGCAAGTGAAGAAAGACAAAGAACATTTGAAGTG	538
Db	541	ACTGATTTTATCAGGGATCTGGCAAGTGAAGAAAGACAAAGAACATCTGAAGTG	600
Qy	539	ATGACGCTGAAGATTAAGTGAAGAAACATGATACAAATG 577	
Db	601	ATGACGCTGAAG-ATTAAGTGAAGAAACATGATACAAATG 638	

RESULT	26
LOCUS	AY399637
DEFINITION	Pan troglodytes HCOM290 gene, virtual transcript, partial sequence.
ACCESSION	AY399637
VERSION	AY399637.1
KEYWORDS	GSS.
SOURCE	Pan troglodytes (chimpanzee)
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;

REFERENCE	TITLE	JOURNAL	PUBMED	REFERENCE	TITLE	JOURNAL	PUBMED
1	Mammalia: Sutheria; Primates: Catarrhini; Homnidae; Pan.			1	1 (bases 1 to 669)		
2	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			2	Adams,M.D. and Cargill,M.		
3	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			3	Science 302 (5652), 1960-1963 (2003)		
4	14671302			4	2 (bases 1 to 669)		
5	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejaival,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.			5	Direct Submision		
6	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			6	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
7	This sequence was made by sequencing genomic exons and ordering them based on alignment.			7	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
8	Location/Qualifiers			8	Location/Qualifiers		

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ORIGIN
/locus_tag="HCN0290"
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	Query Match	81.3%	Score 518.8	IDB 29;	Length 669;
	Best Local Similarity	83.1%	Pred. No. 2.2e-113;		
	Matches 531;	Conservative 0;	Mismatches 107;	Indels 1;	Gaps 1;
Oy	1 ATGTTGGAGCGCTCTTTTTTCTGTGACACTGCCATTCATGCTGAACCTGTGCACCAGT	60			
Dd	1 ATGTTGGAGCGCTCTTTTTTCTGTGACACTGCCATTCATGCTGAACCTGTGCACCAGN	60			
Oy	61 GCAGAAAATGCTTTTAAGTAGACTTAATCAAAACAGCTCTGGAGAGATAAAGCATAT	120			
Dd	61 NNDPAT	120			
Oy	121 GCCTGGAATACCAATGAAGAATACCTCTTCAAAGCAGATGAGCTTCTCCATGAGAAA	180			
Dd	121 GCTGGAGATACCAATGAAGAATACCTCTTCAAAGCAGANNNNNNNNNNNNNNNNNNN	180			
Oy	181 GTTCCCAACAGAGAACACAAGAAATTCCCATGTCTACTCTTGCAATGTAACCAAGG	240			
Dd	181 NNNNNNNNNNNNNNNNNNNNNNNNNNAATTTCCCATGTCTACTCTTGCAATGTAACCAAGG	240			
Oy	241 GTATCATTTCTGTGTGTGTGTTACAGACCCCTTCAAATAACAACCTTCCGCTGTGAG	300			
Dd	241 GTATCATTTCTGTGTGTGTGTTACAGACCCCTTCAAATAACAACCTTCCGCTGTGAG	300			
Oy	301 GTGCATTCAGCCATTAAGATGAACAAGAACCGATCAACATGCTTCTTTCTAATGAC	360			
Dd	301 GTGCATTCAGCCATTAAGATGAACAAGAACCGATCAACATGCTTCTTTCTAATGAC	360			
Oy	361 CAACTCTGAATTTTAAAAATCCTTCCAACATTGACACACCATGAGACCCATCTGTG	420			
Dd	361 CAACTCTGAATTTTAAAAATCCCTTCCAACATTGACACACCATGAGACCCATCTGTG	420			
Oy	421 CCCATCTGATATTAATTAATTTGTGTGAATTTTGTGCATCATCATAGTTGCAATGCACTA	480			
Dd	421 CCCATCTGATATTAATTAATTTGTGTGAATTTTGTGCATCATCATAGTTGCAATGCACTA	480			
Oy	481 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATTTGAATGAT	540			
Dd	481 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATTTGAATGAT	540			
Oy	541 GAGCTGAATAATAGTCTGAAAAACATGATCAATTAATAAATGGCAATCCCTCTGATCCC	600			
Dd	541 GAGCTGAATAATAGTCTGAAAAACATGATCAATTAATAAATGGCAATCCCTCTGATCCC	600			

OY 601 CTGACATGAAGG-GGGCATTTATATGCTTCATG 638
| | | | | | | | | | | | | | | | | | | | | |
Db 601 CTGACATGAAGGAGGGGCATATTATATGATGCCCTTCATG 639

Search completed: June 6, 2004, 14:32:19
Job time : 1618.72 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 6, 2004, 10:27:09 ; Search time 57.8831 Seconds
(without alignments)
6116.792 Million cell updates/sec

Title: US-09-989-724-386_COPY_7_644

Perfect score: 638
Sequence: 1 acgtgtgctgctgctctctt.....attataatgatgcttcatg 638

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 80%
Maximum Match 100%
Listing first 65000 summaries

Database : Issued Patents NA:*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq:*
2: /cgm2_6/ptodata/2/ina/5B COMB.seq:*
3: /cgm2_6/ptodata/2/ina/6A COMB.seq:*
4: /cgm2_6/ptodata/2/ina/6B COMB.seq:*
5: /cgm2_6/ptodata/2/ina/PTUS COMB.seq:*
6: /cgm2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	625	98.0	848	3	US-08-905-223-27
2	625	98.0	848	4	US-09-247-155-27
3	625	98.0	848	4	US-09-663-600A-27
4	625	98.0	848	4	US-09-621-976-5

ALIGNMENTS

RESULT 1
US-08-905-223-27
Sequence 27, Application US/08905223
Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclercq, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905, 223
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israel, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 848 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINEAR
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
DEVELOPMENTAL STAGE: Fetal
TISSUE TYPE: Kidney
FEATURE:
NAME/KEY: sig peptide
LOCATION: 32..73
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 10.7
OTHER INFORMATION: seq LMLFLVLTALHA/EL

US-08-905-223-27

Query Match 98.0%; Score 625; DB 3; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-164;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY	1	ANGTGTGGGCTGCTCTTTTCTGAGTGGCATTCATGCTGAACCTGTCAACAGGT	60
DB	32	ANGTGTGGGCTGCTCTTTTCTGAGTGGCATTCATGCTGAACCTGTCAACAGGT	91
QY	61	GCAGAAATGCTTTAAAGTGAAGTATGATGAGAAAGCTGGAGATTAAGCATAT	120
DB	92	GCAGAAATGCTTTAAAGTGAAGTATGATGAGAAAGCTGGAGATTAAGCATAT	151
QY	121	GCTGGGATTCAGTGAAGTATGCTTTCAAGGATGATGCTTTCTCATGAGAAA	180
DB	152	GCTGGGATTCAGTGAAGTATGCTTTCAAGGATGATGCTTTCTCATGAGAAA	211
QY	181	GTTCCCAAG	240
DB	212	GTTCCCAAG	271
QY	241	GTATCATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCT	300
DB	272	GTATCATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCT	331
QY	301	GTCGATTCAGTGAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	360
DB	332	GTCGATTCAGTGAAGTATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	391
QY	361	CAAGCTGGAATTTTAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	420
DB	392	CAAGCTGGAATTTTAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT	451
QY	421	CCCATCTGATTTATTTATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCT	480
DB	452	CCCATCTGATTTATTTATTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCT	511
QY	481	CTGATTTTATCAGGATCTGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	540
DB	512	CTGATTTTATCAGGATCTGGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	571

QY 541 GACGCTGAAGATTAAGTGTGAAAACATGATCAAAATTGAAAATGGCATCCCTCTGATCCC 600
DB 572 GACGCTGAAGATTAAGTGTGAAAACATGATCAAAATTGAAAATGGCATCCCTCTGATCCC 631
QY 601 CTGACATGAAGGG-GGGCATTTTAAATGATGCTTCATG 638
DB 632 CTGACATGAAGGGGCGCATATTATGATGCTTCATG 670

RESULT 2

US-09-247-155-27
Sequence 27, Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Bouquelier, Lydie
TITLE OF INVENTION: Complementary DNAs
FILE REFERENCE: GENSET.021A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: US/09/247,155A
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER FILING DATE: 1998-02-09
EARLIER APPLICATION NUMBER: 60/081,563
EARLIER FILING DATE: 1998-04-13
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-08-10
EARLIER APPLICATION NUMBER: 60/099,273
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 27
LENGTH: 848
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURES:
NAME/KEY: sig_peptide
LOCATION: 32..73
OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTGGGCTGCTCTTTTCTGTGATGCTGCATTCATGCTGAACCTGTCAACCAAGT 60
DB 32 ATGTGGGCTGCTCTTTTCTGTGATGCTGCATTCATGCTGAACCTGTCAACCAAGT 91
QY 61 GCAGAAATGCTTTTAAAGTGAAGCTTATGATGAGAGCTCTGGAGATTAAGCATAT 120
DB 92 GCAGAAATGCTTTTAAAGTGAAGCTTATGATGAGAGCTCTGGAGATTAAGCATAT 151
QY 121 GCCTGGATACCAATGAAGATACCTCTTCAAGGATGATAGCTTTCTCCATGAGAAA 180
DB 152 GCCTGGATACCAATGAAGATACCTCTTCAAGGATGATAGCTTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTCTTGAATGATTAACCAAGG 240
DB 212 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTCTTGAATGATTAACCAAGG 271
QY 241 GTATCATTTGTTGTGTTAGACACCTTCAAAAATACACCTTCTGCTGTTGAG 300
DB 272 GTATCATTTGTTGTGTTAGACACCTTCAAAAATACACCTTCTGCTGTTGAG 331
QY 301 GTGCAATCAAGCATTAAGATGAACAAGAACCGATCAACAATGCTTTCTTAATGAC 360
DB 332 GTGCAATCAAGCATTAAGATGAACAAGAACCGATCAACAATGCTTTCTTAATGAC 391
QY 361 CAAATCTGAATTTTAAAAATCCCTTCCACATTTGACACCAACCAAGACCATCTGTG 420
DB 392 CAAATCTGAATTTTAAAAATCCCTTCCACATTTGACACCAACCAAGACCATCTGTG 451

QY 421 CCATCTGATTAATTAATTTGTGTGATTAATTTGATCATCATAGTTGCAATGCACTA 480
DB 452 CCATCTGATTAATTAATTTGTGTGATTAATTTGATCATCATAGTTGCAATGCACTA 511
QY 481 CTGATTTTAAAGGATCTGGCAACGTGAAGAAAACAAAGAACATCTGAATGAT 540
DB 512 CTGATTTTAAAGGATCTGGCAACGTGAAGAAAACAAAGAACATCTGAATGAT 571
QY 541 GACGCTGAAGATTAAGTGTGAAAACATGATCAAAATTGAAAATGGCATCCCTCTGATCCC 600
DB 572 GACGCTGAAGATTAAGTGTGAAAACATGATCAAAATTGAAAATGGCATCCCTCTGATCCC 631
QY 601 CTGACATGAAGGG-GGGCATATTATGATGCTTCATG 638
DB 632 CTGACATGAAGGGGCGCATATTATGATGCTTCATG 670

RESULT 3

US-09-663-600A-27
Sequence 27, Application US/0963600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Bouquelier, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 27
LENGTH: 848
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURES:
NAME/KEY: sig_peptide
LOCATION: 32..73
OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 ATGTGGGCTGCTCTTTTCTGTGATGCTGCATTCATGCTGAACCTGTCAACCAAGT 60
DB 32 ATGTGGGCTGCTCTTTTCTGTGATGCTGCATTCATGCTGAACCTGTCAACCAAGT 91
QY 61 GCAGAAATGCTTTTAAAGTGAAGCTTATGATGAGAGCTCTGGAGATTAAGCATAT 120
DB 92 GCAGAAATGCTTTTAAAGTGAAGCTTATGATGAGAGCTCTGGAGATTAAGCATAT 151
QY 121 GCCTGGATACCAATGAAGATACCTCTTCAAGGATGATAGCTTTCTCCATGAGAAA 180
DB 152 GCCTGGATACCAATGAAGATACCTCTTCAAGGATGATAGCTTTCTCCATGAGAAA 211
QY 181 GTTCCCAACAGAGAGCAAGAAATTTCCATGCTCTTGAATGATTAACCAAGG 240

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Db 212 GTTCCACAGAGAGAACACAGAAATTTCCATGTCCTTTCATGATGAATCCAGAGG 271
Qy 241 GATACATTCGTGTTGTGTTACAGACCCCTTCAAAAATACACCCCTCTGCTGTTGAG 300
Db 272 GATACATTCGTGTTGTGTTACAGACCCCTTCAAAAATACACCCCTCTGCTGTTGAG 331
Qy 301 GTGCATCAGCCCTAAGATGAAACAAGAACCGATACAAATGCTCTTCTTAATGAC 360
Db 332 GTGCATCAGCCCTAAGATGAAACAAGAACCGATACAAATGCTCTTCTTAATGAC 391
Qy 361 CAACCTGGAATTTTAAATAATCCCTCCACACTTGACACCCAGTGAACCATCTGAG 420
Db 392 CAACCTGGAATTTTAAATAATCCCTCCACACTTGACACCCAGTGAACCATCTGAG 451
Qy 421 CCCATCTGATTAATTAATTTGTGATATTTTGCATCATCAATGATGCAATGCACTA 480
Db 452 CCCATCTGATTAATTAATTTGTGATATTTTGCATCATCAATGATGCAATGCACTA 511
Qy 481 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAAACCAATCTGAAGTGAT 540
Db 512 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAAACCAATCTGAAGTGAT 571
Qy 541 GAGCTGAAGATTAAGTGTGAAAACATGATCACAATTGAAAATGSCATCCCTGATCCC 600
Db 572 GAGCTGAAGATTAAGTGTGAAAACATGATCACAATTGAAAATGSCATCCCTGATCCC 631
Qy 601 CTGACATGAAGGG-GGGCATTAATTAATGATGCTTCATG 638
Db 632 CTGACATGAAGGGAGGGCATTAATTAATGATGCTTCATG 670
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RESULT 4
US-09-621-976-5

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; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET. 054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..697
; NAME/KEY: 819 peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5
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Query Match 98.0%; Score 625; DB 4; Length 848;
Best Local Similarity 99.2%; Pred. No. 1.2e-184;
Matches 634; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

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Qy 1 AAGTTGAGCTGCTCTTTTCTGAGCTGCAATTCAGTCACTCTGTCAACCAAGT 60
Db 32 AAGTTGAGCTGCTCTTTTCTGAGCTGCAATTCAGTCACTCTGTCAACCAAGT 91
Qy 61 GCAGAAATGCTTTTAAAGAGACTTATGATCAGAACAGCTCGGAGATAAGCATAT 120
Db 92 GCAGAAATGCTTTTAAAGAGACTTATGATCAGAACAGCTCGGAGATAAGCATAT 151
Qy 121 GCCTGGATACCAATGATACCTCTTCAAGCGATGATGCTTCTCATGAGAAA 180
Db 152 GCCTGGATACCAATGATACCTCTTCAAGCGATGATGCTTCTCATGAGAAA 211
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Qy 181 GTTCCACAGAGAGAACACAGAAATTTCCATGTCCTTTCATGATGAATCCAGAGG 240
Db 212 GTTCCACAGAGAGAACACAGAAATTTCCATGTCCTTTCATGATGAATCCAGAGG 271
Qy 241 GATACATTCGTGTTGTGTTACAGACCCCTTCAAAAATACACCCCTCTGCTGTTGAG 300
Db 272 GATACATTCGTGTTGTGTTACAGACCCCTTCAAAAATACACCCCTCTGCTGTTGAG 331
Qy 301 GTGCATCAGCCCTAAGATGAAACAAGAACCGATACAAATGCTCTTCTTAATGAC 360
Db 332 GTGCATCAGCCCTAAGATGAAACAAGAACCGATACAAATGCTCTTCTTAATGAC 391
Qy 361 CAACCTGGAATTTTAAATAATCCCTCCACACTTGACACCCAGTGAACCATCTGAG 420
Db 392 CAACCTGGAATTTTAAATAATCCCTCCACACTTGACACCCAGTGAACCATCTGAG 451
Qy 421 CCCATCTGATTAATTAATTTGTGATATTTTGCATCATCAATGATGCAATGCACTA 480
Db 452 CCCATCTGATTAATTAATTTGTGATATTTTGCATCATCAATGATGCAATGCACTA 511
Qy 481 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAAACCAATCTGAAGTGAT 540
Db 512 CTGATTTTATCAGGATCTGGCAACGTAGAGAAAGAAACCAATCTGAAGTGAT 571
Qy 541 GAGCTGAAGATTAAGTGTGAAAACATGATCACAATTGAAAATGSCATCCCTGATCCC 600
Db 572 GAGCTGAAGATTAAGTGTGAAAACATGATCACAATTGAAAATGSCATCCCTGATCCC 631
Qy 601 CTGACATGAAGGG-GGGCATTAATTAATGATGCTTCATG 638
Db 632 CTGACATGAAGGGAGGGCATTAATTAATGATGCTTCATG 670
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Search completed: June 6, 2004, 13:08:30
Job time: 60.8831 secs